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TO: Michael Borin **Location: 12a 01 / 12d01** **Wednesday, July 16, 2003** **Art Unit: 1631** **Phone: 308-4506** **Serial Number: 09 / 586529**	**From: Jan Delaval** **Location: Biotech-Chem Library** **CM1-1E07** **Phone: 308-4498** **jan.delaval@uspto.gov**

Search Notes

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To: Jan Delaval 97964

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: M. Berin Examiner #: 74104 Date: 07/02

Art Unit: 1631 Phone Number 305-4506 Serial Number: 09/586529

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If more than one search is submitted, please prioritize searches in order of need.

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

***For Sequence Searches Only** Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search claims 1, 2, 10, 24, 25

Thank you :-)

M. Berin

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Searcher Prep & Review Time: _____

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Online Time: +150

Type of Search

NA Sequence (#) _____

AA Sequence (#) _____

Structure (#) _____

Bibliographic ✓

Litigation _____

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Patent Family _____

Other _____

Vendors and cost where applicable

STN ✓

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis _____

Sequence Systems _____

WWW/Internet _____

Other (specify) _____

PTO-1590 (8-01)

STIC SEARCH RESULTS

USPTO

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

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- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art **not found:***
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

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L25  ANSWER 1 OF 8  WPIX   (C) 2003 THOMSON DERWENT
AN   2002-590755 [63]   WPIX
DNC  C2002-167209
TI   Identifying oligonucleotide sequences for amplifying a unique sequence
     within a genomic region, useful for producing unique, repeat-free probes,
     comprises identifying repeat sequence-free subregions within a genomic
     region.
DC   B04 D16
IN   ALBERTSON, D G; COLLINS, C; GRAY, J W; PINKEL, D;
     VOLIK, S; VOLIK, S V
PA   (ALBE-I) ALBERTSON D G; (COLL-I) COLLINS C; (GRAY-I) GRAY J W; (PINK-I)
     PINKEL D; (VOLI-I) VOLIK S; (REGC) UNIV CALIFORNIA
CYC  100
PI   WO 2002057481 A2 20020725 (200263)* EN   30p    C12Q000-00      <--
        RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
            NL OA PT SD SE SL SZ TR TZ UG ZM ZW
         W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
            DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
            KZ LC LK LR LS LT LU LV MA MD MG MK MN M                        T
            RO RU SD SE SG SI SK SL TJ TM TN TR TT T                        W
     US 2003022166 A1 20030130 (200311)
ADT  WO 2002057481 A2 WO 2002-US365 20020107; US 200                        0
     20010119
PRAI US 2001-766450   20010119
IC   ICM  C12Q000-00; C12Q001-68
     ICS  C07H021-04; G01N033-48; G01N033-50; G06F01
AB   WO 200257481 A UPAB: 20021001
     NOVELTY - Identifying (M1) oligonucleotide seque                      g
     repeat sequence-free subsequences within the genomic region of interest to
     a nucleotide sequence database, to identify nucleotide sequences within
     the nucleotide sequence database that are substantially similar to the
     repeat sequence-free subsequences, is new.
          DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:
          (1) identifying (M2) oligonucleotide sequences for amplifying a
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Because of date limitation, I could not find a really outstanding ref for 102

unique sequence within a genomic region of interest, comprises:

(a) executing a first process on a digital computer to identify repeat sequences that occur within the genomic region of interest;

(b) executing a second process on a digital computer to compare repeat sequence-free subsequences within the genomic region of interest to a nucleotide sequence database, where nucleotide sequences within the nucleotide sequence database that are substantially similar to the repeat sequence-free subsequences are identified;

(c) executing a third process on a digital computer to identify oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within any of the repeat sequence-free subsequences for which a defined number of substantially similar sequences are identified in the nucleotide sequence database; and

(d) outputting the oligonucleotide sequences;

(2) identifying (M3) oligonucleotide sequences for amplifying a unique sequence within a genomic region of interest comprising:

(a) analyzing a genomic nucleotide sequence that encompasses the genomic region of interest to identify repeat sequences within the genomic region;

(b) comparing at least one repeat sequence-free subsequence within the genomic nucleotide sequence to a nucleotide sequence database to identify sequences within the database that are substantially similar to the repeat sequence-free subsequence;

(c) for at least one of the repeat sequence-free subsequences for which a defined number of substantially similar sequences are identified within the nucleotide sequence database, selecting oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within the repeat sequence-free subsequence;

(3) a computer program product designing and outputting oligonucleotide sequences suitable for use as primers to amplify unique sequences within a genomic region of interest, comprising a storage structure having computer program code embodied within, where the computer program code comprises:

(a) computer program code for analyzing a nucleotide sequence encompassing the genomic region of interest to identify repeat sequences within the nucleotide sequence;

(b) computer program code, which for each subsequence of the nucleotide sequence that does not contain any of the repeat sequences, compare the subsequence against a nucleotide sequence database to identify nucleotide sequences within the database that are substantially similar to the subsequence;

(c) a computer program code which identifies oligonucleotide sequences suitable for use as primers in an amplification reaction to amplify a product within the subsequence, for each of the subsequences for which a defined number of substantially similar sequences are found in the database, and

(d) computer program code for outputting the oligonucleotide sequences; and

(4) identifying (M4) genes within a genomic region of interest comprising:

(a) executing a first process on a digital computer to identify repeat sequences that occur within the genomic region of interest;

(b) executing a second process on a digital computer to compare repeat sequence-free subsequences within the genomic region of interest to a nucleotide sequence database, where nucleotide sequences within the nucleotide sequence database that are substantially similar to the repeat sequence-flee subsequences are identified;

(c) executing a third process on a digital computer to select repeat sequence-free subsequences having no substantially similar sequences to identify a repeat sequence-free subsequence may represent a gene family;

(d) identify oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within any of the repeat sequence-free subsequences for which a defined number of

substantially similar sequences are identified in the nucleotide sequence database; and

(e) outputting the oligonucleotide sequences.

USE - (M1) is useful for identifying oligonucleotide sequences for amplifying a unique sequence within a genomic region, and for producing unique, repeat-free probes which represent truly unique sequences within the genome. (M1) is also useful for the identification of candidate genes within a genetic interval, and in the identification of potential coding sequences within the region. Those sequences found to lack both known repetitive sequences as well as close homologs in the genome may be used to design primers that would allow amplification of unique products for use as probes or array targets. The probes or array targets can be used without adding an excess of additional unlabeled repeat sequences for enhancing the speed, simplicity, and efficiency of the reaction compared to traditional methods.

ADVANTAGE - (M1) is rapid, efficient, and automated for identifying unique sequences within the genome. (M1) is inherently high-throughput and easy to automate, and is independent of any bias towards previously identified expressed sequences.

Dwg.0/2

FS CPI

FA AB; DCN

MC CPI: B04-B03C; **B04-E05**; B11-C08E3; B11-C08E5; B11-C08E6; **B11-C08F1**; **B12-K04F**; D05-H09; **D05-H12D**; **D05-H12D1**; **D05-H18B**

TECH UPTX: 20021001

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The genomic region is from a human genome. The number of substantially similar sequences is zero. The oligonucleotide sequences are outputted by displaying the sequences on a computer screen or on a computer printout, or by executing a fourth process on a digital computer to direct the synthesis of oligonucleotide primers comprising the oligonucleotide sequences. The computer directs the synthesis of the oligonucleotide primers by ordering the synthesis from an external source, and is in communication with an oligonucleotide synthesizer, which directs the synthesis of the oligonucleotide primers. The substantially similar sequences are at least 50-90% identical to the repeat sequence-free subsequences. The first process is executed using Repeat Masker software, a Basic local alignment search tool (BLAST) algorithm or a Primer3 software. (M2) further comprises producing an amplification product using the oligonucleotide primers, where the amplification product is a FISH probe, preferably fluorescently labeled, or is an array CGH target. (M3) further comprises displaying the oligonucleotide sequences on a computer screen or on a computer printout, and directing the synthesis of oligonucleotide primers comprising the oligonucleotide sequences by ordering the synthesis of the primers from an external source.

L25 ANSWER 2 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN **2002-303417** [34] WPIX

CR 1991-165919 [23]; 1992-217417 [27]; 1992-286380 [35]; 1993-303497 [38]; 1995-319885 [41]; 1999-037064 [04]; 1999-105095 [09]; 1999-579905 [49]; 1999-619646 [53]; 2001-564345 [63]; 2002-163200 [21]; 2003-352179 [33]; 2003-352608 [33]

DNC **C2002-088220**

TI Comparative genomic hybridization to determine relative copy numbers of nucleotide sequences in subject and reference genomes as functions of locations, by comparing signal intensities of subject and reference genes.

DC B04 D16

IN **GRAY, J W**; KALLIONIEMI, A; KALLIONIEMI, O; PINKEL, D; SAKAMOTO, M; WALDMAN, F

PA (REGC) UNIV CALIFORNIA

CYC 1

PI US 2002028460 A1 20020307 (200234)* 52p C12Q001-68

ADT US 2002028460 A1 CIP of US 1991-696948 19910508, CIP of US 1992-846659 19920304, Cont of US 1993-132172 19931006, Div ex US 1994-223905 19940406, Cont of US 1995-565304 19951127, Cont of US 1999-311835 19990514, US 2001-912818 20010724

FDT US 2002028460 A1 Cont of US 5976790

PRAI US 1993-132172 19931006; US 1991-696948 19910508; US 1992-846659 19920304; US 1994-223905 19940406; US 1995-565304 19951127; US 1999-311835 19990514; US 2001-912818 20010724

IC ICM C12Q001-68
ICS C12P019-34

AB US2002028460 A UPAB: 20030526

NOVELTY - Comparative genomic hybridization (CGH) (M1) for determining relative copies of nucleic acid sequence in one or more subject genomes or its portions as a function of the location of those sequences in a reference genome involves comparing intensities of the signals from each labeled subject nucleic acid and/or the differences in the ratios between different signals from the labeled sequences.

DETAILED DESCRIPTION - In M1, comparing copy numbers of different DNA or RNA sequences in a subject cell or cell population involves:

(a) extracting the DNA or RNA from the subject cell or from a number of cells of the subject cell population;

(b) amplifying the extracted subject DNA or RNA, if necessary;

(c) labeling the subject DNA or RNA;

(d) hybridizing the labeled subject DNA or RNA in situ to reference metaphase chromosomes after substantially removing from the labeled DNA or RNA those repetitive sequences that could bind to multiple loci in the reference metaphase chromosomes, and/or after blocking the binding sites for those repetitive sequences in the reference metaphase chromosomes by prehybridization with appropriate blocking nucleic acids, and/or blocking those repetitive sequences in the labeled DNA or RNA by prehybridization with appropriate blocking nucleic acid sequences, and/or including such blocking nucleic acid sequences for the repetitive sequences during the hybridization, where the DNA or RNA sequences in the labeled subject DNA or RNA that bind to single copy sequences in the reference metaphase chromosomes are substantially retained, and those single copy DNA or RNA sequences as well as their binding sites in the reference metaphase chromosomes remain substantially unblocked both before and during the hybridization;

(e) rendering the bound, labeled DNA or RNA sequences visualizable, if necessary;

(f) observing and/or measuring the intensity of the signal from the labeled subject DNA or RNA sequences as a function of position on the reference metaphase chromosomes; and

(g) comparing the copy numbers of different DNA or RNA sequences of the subject DNA or RNA by comparing the signal intensities at different positions on the reference metaphase chromosomes, where the greater the signal intensity at a given position, the greater the copy number of the sequences in the subject DNA or RNA that bind at that position.

INDEPENDENT CLAIMS are also included for the following:

(1) quantitatively comparing (M2) copy numbers of different DNA sequences in one subject cell or cell population relative to copy numbers of substantially identical sequences in another subject cell or cell population;

(2) determining (M3) the ratio of copy numbers of different DNA sequences in one subject cell or cell population to copy numbers of substantially identical sequences in another cell or cell population; and

(3) detecting (M4) amplification of a certain sequence or group of sequences in a subject cell or cell population.

USE - M1 is useful for comparing copy numbers of different DNA or RNA sequences in a subject cell or cell population (claimed). M1 is useful for finding regions in normal genomes which when altered in sequence copy number contribute to diseases such as cancer or birth defects, to detect sequence copy number imbalances throughout an entire genome in one

hybridization, to map gains and/or losses of sequences in a genome and/or to provide a copy number karyotype of a subject genome, for prenatal or perinatal analysis, for identifying previously unknown regions of amplification and/or deletion, to assess the association between gene amplification and/or deletion and the extent of tumor evolution, and to identify amplification and/or deletion events that are associated with drug resistance.

ADVANTAGE - M1 enables rapid identification of only those copy number changes that occurred in most of the cells.

DESCRIPTION OF DRAWING(S) - The figure shows the general approach used in preforming CGH (Comparative genomic hybridization).

Dwg.2/20

FS CPI

FA AB; GI; DCN

MC CPI: **B04-E01**; B11-C07B3; B11-C08E3; B11-C08E5; **B11-C08F** ; B12-K04A; **B12-K04F**; D05-H09; **D05-H18B**

TECH UPTX: 20020528

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: In M1, the repetitive sequences that could bind to multiple loci in the reference metaphase chromosomes are high copy number repetitive sequences. The subject cell or cell population is derived from a clinical specimen. The subject DNA is extracted from formalin-fixed and/or paraffin-embedded archived tissue specimens. The copy number of a subject DNA sequence binding at one position in the reference metaphase chromosomes relative to the copy number of a sequence binding at another position is quantified by measuring the ratio of the signal intensities at the 2 locations. M1 further comprises the addition of an unlabeled nucleic acid to the hybridization mixture, where the unlabeled nucleic acid has a sufficient number of nucleic acid sequences substantially complementary to the sequences in the reference metaphase chromosomes to prevent saturation of the binding sites in the reference metaphase chromosomes by the labeled subject DNA. The reference metaphase chromosomes are human and prehybridized with human genomic DNA and/or human genomic DNA enriched in high copy repetitive sequences, and are included in the hybridization. The labeled subject DNA is tumor or fetal DNA.

ABEX UPTX: 20020528

EXAMPLE - Comparative genomic hybridization (CGH) to identify and map increases in DNA sequence copy number in 15 breast cancer cell lines was as follows. 15 breast cancer cell lines such as BT-20, BT-474, BT-483, MCF7, MDA-157, MDA-175, MDA-231, MDA-330, MDA-361, MDA-435, MDA-436, MDA-453, SK-BR-3, ZR-75-1, ZR-75-30 were obtained. The cells were grown, trypsinized, suspended in a digestion buffer, incubated and high molecular weight DNA was extracted. DNA was also isolated from the peripheral blood of 7 normal healthy individuals. One of these was used as the normal reference DNA is all CGH hybridizations. The target metaphase slides were prepared from PHA-stimulated peripheral blood lymphocytes from a normal male. To assess the hybridization characteristics, each batch of slides was extensively tested with labeled normal genomic DNA and with whole-chromosome painting probes. CGH was performed essentially as described above. DNA samples were labeled either with biotin-14-dATP (test samples) or digoxigenin-11-dUTP (normal reference DNA). 60-100 ng of each of the labeled probes and 5 microg of unlabeled Cot-1 DNA were precipitated. The DNAs were dissolved in 10 microl of hybridization buffer. Metaphase slides were denatured, dehydrated, treated with proteinase K and dehydrated again. The hybridization mixture was applied on slides and hybridized and after hybridization, the slides were washed. Biotinylated DNA was detected with 5 microg/ml Avidin-fluorescein isothiocyanate (FITC) and digoxigenin-labeled DNA with 1 microg/ml anti-digoxigenin Rhodamine. The hybridization were analyzed using a digital image analysis system. 5 metaphases from each hybridization were analyzed for the chromosomal locations of DNA sequence increases. These regions were determined using green to red fluorescence intensity ratio profiles and information was gained during visual inspection of the

digital images. Criteria used to define the increased DNA sequence copy number in tumors were based on comparisons of normal DNAs labeled and stained with 2 different colors. These included green to red ratios that exceeded 1.25 or small paired spots of green fluorescence clearly above the background. High-level increases were defined as those chromosomal subregions where the green to red ratio exceeded 1.75. Increases that were not systematically present in all metaphases or that were seen only in one chromatid or in one of the 2 chromosome homologs were considered non-specific and were excluded from analysis. Interpretation of CGH data was guided by control experiments. Comparisons among 7 normal DNA specimens were used to establish normal levels of green to red fluorescence intensity ratio variation along the length of all human chromosomes while cell lines with known amplifications were used to assess sensitivity. 4-6 breast cancer cell lines with known ERBB2 amplification and 3 of 5 with known BCL1 amplification showed evidence of increased copy number by CGH at 17q12 and 11q13, as expected. All high level amplifications were detected by CGH, while those of a lower level were missed. No false positive ERBB2 or BCL1 amplifications were seen.

L25 ANSWER 3 OF 8 WPIX (C) 2003 THOMSON DERWENT
AN **2002-114358** [15] WPIX
DNC **C2002-035107**
TI New method of comparing test and reference genome in identifying rearrangement in tumor genomes comprising sequencing the ends of obtained inserts from the test genome and comparing the co-linearity of the ends with corresponding sequences.
DC B04 D16
IN **COLLINS, C; GRAY, J W; VOLIK, S**
PA (REGC) UNIV CALIFORNIA
CYC 96
PI WO 2001092558 A2 20011206 (200215)* EN 38p C12Q000-00 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001075110 A 20011211 (200225) C12Q000-00
ADT WO 2001092558 A2 WO 2001-US17757 20010531; AU 2001075110 A AU 2001-75110 20010531
FDT AU 2001075110 A Based on WO 200192558
PRAI US 2000-586529 20000531
IC ICM C12Q000-00
AB WO 200192558 A UPAB: 20020306
NOVELTY - Comparing, (M1), a test genome to a reference genome involves generating or obtaining a large insert vector library from a test genome, sequencing the ends of the inserts in the library and comparing the co-linearity of the sequenced ends in the library with corresponding sequences within a substantially sequenced reference genome, is new.

DETAILED DESCRIPTION - Comparing, M1, a test genome to a reference genome comprising:

(i) providing several clones of known size that covers at least a portion of the test genome;

(ii) obtaining sequence information from the termini of each of the clone thus obtaining a pair of terminal sequences;

(iii) identifying a pair of sequences within the reference genome that corresponds to each of the pairs of the terminal sequences; and

(iv) determining the relationship between the members of each pair of corresponding sequences within the reference genome.

A pair of terminal sequences is also obtained by obtaining a subset of the clones, fractionating the clones inserts, generating several subclones and obtaining sequence information from each of the subclones. A difference in the observed relationship between the members of any of the

pairs of corresponding sequences within the reference genome and the expected relationship based upon the known size of the clones indicates the presence of a rearrangement in the test genome compared to the reference genome.

USE - For identifying rearrangement in tumor genomes and for determining genetic differences between closely related species as well as between different strains of the same species.

ADVANTAGE - The method rapidly identifies rearrangements within test genomes e.g. a tumor genome in comparison with a substantially-sequenced reference genome. The method represents a major improvement over previous methods in terms of efficiency, rapidity and cost-effectiveness.

Dwg.0/0

FS CPI

FA AB; DCN

MC CPI: **B04-E01**; **B04-E05**; B04-F0100E; B04-F02A; **B11-C08F**; B12-K04A1; B12-K04E; D05-H09; **D05-H12**; **D05-H12D1**; D05-H14B2; **D05-H18**

TECH UPTX: 20020306

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The method further involves determining the sequence of the test genome over a region spanning at least one breakpoint of the rearrangement. The clones cover substantially all the test genome. The method further involves determining the frequency of each of the terminal sequences within the clones where an increased or decreased relative frequency of the terminal sequences indicates the presence of amplification or deletion in the test genome that includes the terminal sequence. Preferred Genome: The reference and the test genomes are from different species. The reference genome is a human genome. The test genome is from tumor cell. The terminal sequences are determined by automated sequencing. The pairs of terminal sequences from the test genome are compared to the pairs of corresponding sequence within the reference genome using a computer. Preferred Members: The members of at least one pair of corresponding sequences within the reference genome are closer together or apart than expected based on the known size of the clones, indicating the presence of an insertion or deletion respectively in the test genome between the pair of terminal sequences corresponding to the at least one pair of corresponding sequence. The members of at least one pair of corresponding sequences within the reference genome are present on different chromosomes within the reference genome, indicating the presence of a translocation in the test genome between the pair of terminal sequences corresponding to the at least one pair of corresponding sequences. Preferred Clones: The clones are BAC or PAC clones. The clones represent a redundancy of at lest about 10 (preferably 20) fold of the test genome or the portion of the test genome. The clones contain at least about 100000 (preferably 200000, particularly 250000) clones. The subclones represent a redundancy of 0.001 - 5 (preferably 0.01 - 1, more preferably 0.05 - 0.5, particularly 0.1) fold of the subset of the clones. Preferred Sequences: The terminal sequences are present on average between about 5 - 500 (preferably at most50, more preferably at most10, particularly at most5) kb throughout the test genome or the portion of the test genome. The sequence is obtained from the termini of each of the subclones.

ABEX UPTX: 20020306

EXAMPLE - No relevant example given.

L25 ANSWER 4 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN 2002-114015 [15] WPIX

DNN N2002-085067 DNC C2002-034865

TI A new software tool for integration and presentation of repeat and CpG dinucleotide distribution in a DNA sequence provides a graphical output useful in functional genomic analysis.

DC B04 D16 P85 T01

IN **COLLINS, C; GRAY, J W; VOLIK, S**

PA (REGC) UNIV CALIFORNIA

CYC 94
PI WO 2001075856 A1 20011011 (200215)* EN 20p G09G005-36 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ
LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD
SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2001049701 A 20011015 (200215) G09G005-36
ADT WO 2001075856 A1 WO 2001-US10399 20010330; AU 2001049701 A AU 2001-49701 20010330
FDT AU 2001049701 A Based on WO 200175856
PRAI US 2000-541438 20000331
IC ICM G09G005-36
ICS **C12Q001-68**
AB WO 200175856 A UPAB: 20020306
NOVELTY - Analyzing and displaying on a digital computer a sequence of base pairs, and plotting descriptive information regarding the sequence, is new.

DETAILED DESCRIPTION - Analyzing and displaying on a digital computer a sequence comprising a list of base pairs, and plotting descriptive information regarding the sequence comprises:

(a) executing a process to identify repeat sequences in the sequence;

(b) plotting an axis corresponding to the sequence base pairs, in windows of specified number of base pair units; and

(c) for each window, plotting along a second axis an indication of the portion of the base pairs included in the window that comprise repeat sequences.

INDEPENDENT CLAIMS are also included for the following:

(1) visualizing features of a nucleotide sequence, comprising:

(a) dividing the sequence into contiguous windows with a width of chosen numbers of base pairs;

(b) analyzing the sequence to identify repeat data;

(c) generating repeat frequency information in each window;

(d) generating CpG frequency output files for each window;

(e) providing a masked sequence having repeat data masked from the sequence;

(f) selecting a sequence database including previously determined sequences;

(g) comparing the masked sequence to the database to create a database hit output file identifying regions of the sequence database that align with portions of the masked sequence;

(h) analyzing the database output files to create a list of the number of relevant hits for each window;

(i) capturing those hits which extend over length and identity over a selected threshold of base pairs and generating annotation data;

(j) gathering repeat information from the repeat output files, annotation and distribution of database hits and producing a graphical summary for display or reproduction; and

(k) plotting frequency of CpG and gene-indicating sequences on the summary;

(2) visually displaying selected information about a DNA sequence comprising:

(a) analyzing the sequence to identify regions of repeat data;

(b) using the identified regions to form a masked sequence;

(c) performing an alignment search of the masked sequence on a selected sequence database to generate alignment information;

(d) analyzing the alignment information to determine regions of correspondence of a specified type;

(e) plotting graphical regions indicating the correspondence;

(f) analyzing the sequence data to determine frequency of selected nucleotide pairs; and

(g) graphically indicating the above frequency and the proportion of

the window containing the repeat data;

(3) a computer program visualizing important features of a genome sequence for processing repeat data and indicating regions of correspondence between sequences in a database comprising code for carrying out the processes as detailed in the disclosure.

USE - The software is used in the functional interpretation of DNA sequences especially the number of short interspersed repetitive elements, long interspersed repetitive elements, long terminal repeats, DNA elements, satellites, simple repeats and low complexity regions.

ADVANTAGE - Unlike prior art programs the output is in graphical form, compressing 400-500 pages of text output to 4-5 pages of easy to analyze graphical summary.

Dwg.0/3

FS CPI EPI GMPI

FA AB; DCN

MC CPI: **B04-E01**; B11-C08E5; **B12-K04F**; D05-H09; **D05-H12**
EPI: **T01-J05B2**; **T01-J05B4P**; **T01-J12B1**; **T01-S03**

TECH UPTX: 20020306

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The method preferably includes a second process to determine frequency of occurrence in each window of a specified nucleotide pair, particularly CpG dinucleotides, and plotting their frequency. The first process preferably includes determining the number of short interspersed repetitive elements, long interspersed repetitive elements, long terminal repeats, DNA elements, satellites, simple repeats and low complexity regions, and plotting each number.

ABEX UPTX: 20020306

EXAMPLE - No suitable example is given.

L25 ANSWER 5 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN 2000-224375 [19] WPIX

DNC C2000-068544

TI Identification of novel amplicons in human chromosome 20 for diagnosis and prognosis of cancers, particularly breast cancer, involves hybridization of a probe specific for this region.

DC B04 D16

IN ALBERTSON, D; **COLLINS, C**; **GRAY, J**; PINKEL, D; ALBERTSON, D G; **GRAY, J W**

PA (REGC) UNIV CALIFORNIA; (ALBE-I) ALBERTSON D G; (COLL-I) COLLINS C; (GRAY-I) GRAY J W; (PINK-I) PINKEL D

CYC 22

PI WO 2000009758 A1 20000224 (200019)* EN 48p C12Q001-68 <--
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP
EP 1112379 A1 20010704 (200138) EN C12Q001-68 <--
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
US 2002120526 A1 20020829 (200259) G06F017-60 <--
JP 2002522097 W 20020723 (200263) 64p C12Q001-68 <--

ADT WO 2000009758 A1 WO 1999-US18483 19990812; EP 1112379 A1 EP 1999-941131 19990812, WO 1999-US18483 19990812; US 2002120526 A1 Div ex US 1998-134044 19980814, US 2001-896070 20010628; JP 2002522097 W WO 1999-US18483 19990812, JP 2000-565192 19990812

FDT EP 1112379 A1 Based on WO 200009758; JP 2002522097 W Based on WO 200009758

PRAI US 1998-134044 19980814; US 2001-896070 20010628

IC ICM **C12Q001-68**; **G06F017-60**
ICS C12N015-09; G01N033-53; G01N033-566; G01N037-00

AB WO 200009758 A UPAB: 20000419

NOVELTY - Screening for an amplicon in a sample human nucleic acid (A) comprises detecting a hybridization complex formed by contacting (A) with a probe that specifically hybridizes to a nucleic acid sequence (I) including D20S211 through D20S120.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a nucleic acid probe comprising a sequence which specifically hybridizes to (I); and

(2) a kit for screening the presence of an amplicon comprising (I) comprising probes as in (1).

USE - The screening methods are useful for identifying amplicons in a human nucleic acid sample which are used for diagnosing and prognosing cancers, particularly breast cancers.

DESCRIPTION OF DRAWING(S) - The figure shows the results of an analysis of the 20q13.2 region of a tumor (S21) using hybridoma analysis. The graphs show comparative genomic hybridization (CGH) ratios for selected 20q13.2 clones in tumor S21, indicating the G/R or green (fluorescine dCTP) to red (Texas red dCTP) fluorescence ratio as a function of the amount of genomic nucleic acid hybridization to the 20q13.2 contig clones.

Dwg.1/3

FS CPI

FA AB; GI; DCN

MC CPI: **B04-E05**; B11-C08E5; B12-K04E; **B12-K04F**; **D05-H12D1**; **D05-H18B**

TECH UPTX: 20000419

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The human nucleic acid is genomic DNA isolated from breast tumor cells. Detection further involves determining the copy number of the amplicon. (A) and (I) are labeled with a detectable composition (preferably fluorescein or Texas red for (A)). The method further comprises providing a nucleic acid from a reference cell which is contacted with the probe before or simultaneously with (A) and/or hybridizing CotI DNA to (A) before contacting (A) with (I).

Preferred Nucleic Acid: (I) comprises a Genome Database (GDB) locus nucleic acid sequence (Ia) (comprising 1 of 7 sequences named in the specification, e.g. D20S211), a cloned genomic nucleic acid sequence (Ib) (comprising 1 of 16 sequences named in the specification, e.g. RMC20B4097) or a polymerase chain reaction primer pair comprising STS marker sequence (Ic) (comprising 1 of 10 sequences named in the specification, e.g. AFMa233wgl). (I) is preferably attached to solid surface as a member of a nucleic acid array.

ABEX UPTX: 20000419

SPECIFIC OLIGONUCLEOTIDES - (I) comprises a Genome Database (GDB) locus nucleic acid sequence (Ia), a cloned genomic nucleic acid sequence (Ib), or a polymerase chain reaction primer pair comprising STS marker sequence (Ic).

(Ia) is D20S211, D20S854, D20S876, D20S1044, D20S913, D20S720 and D20S120. (Ib) is RMC20B4097, RMC20B4103, RMC20P4016, RMC20B4130, RMC20P4185, RMC20B4188, RMC20B4109, RMC20P4010, RMC20P4028, RMC20P4003, RMC20B4099, RMC20P4018, RMC20P4069, RMC20B4121, RMC20B4087 and RMC20P4070. (Ic) is AFMa233wgl, AFM080yal, AFM069yal, WI-16748, WI-9939, AFMa072zb9, WI-6578, AFM224zd12, WI-9227 and AFM276xh1 (claimed).

EXAMPLE - Nucleic acid from breast tissue was used to prepare labeled biological sample, the cloned genomic DNA use as probes was produced by standard recombinant technology. A standard hybridization reaction was performed using fluorescein labeled human nucleic acid and Texas red labeled DNA. After hybridization the slide was washed and placed in an array apparatus for reading fluorescence. The data obtained from the intensities of two fluorochromes was calculated for each target and the data was transmitted for storage and analysis by an image analysis program.

L25 ANSWER 6 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN **1999-579905** [49] WPIX

CR 1991-165919 [23]; 1992-217417 [27]; 1992-286380 [35]; 1993-303497 [38];

1995-319885 [41]; 1999-037064 [04]; 1999-105095 [09]; 1999-619646 [53]; 2001-564345 [63]; 2002-163200 [21]; 2002-303417 [34]; 2003-352179 [33]; 2003-352608 [33]

DNC **C1999-168669**

TI Detecting an amplification of sequences using comparative genomic hybridization.

DC B04 D16

IN **GRAY, J W**; KALLIONIEMI, A; KALLIONIEMI, O; PINKEL, D; SAKAMOTO, M; WALDMAN, F

PA (REGC) UNIV CALIFORNIA

CYC 1

PI US 5965362 A 19991012 (199949)* 54p C12Q001-68

ADT US 5965362 A CIP of US 1992-846659 19920304, CIP of US 1992-969948 19921030, Cont of US 1993-132172 19931006, Div ex US 1994-223905 19940406, US 1995-562965 19951127

PRAI US 1993-132172 19931006; US 1992-846659 19920304; US 1992-969948 19921030; US 1994-223905 19940406; US 1995-562965 19951127

IC ICM C12Q001-68
ICS A61K049-00; C07H021-02; C12P019-34

AB US 5965362 A UPAB: 20030526
NOVELTY - A method, known as comparative genomic hybridization (CGH), to compare the copy numbers of different DNA/RNA sequences from a sample by using kinetics of in situ hybridization, is new.

DETAILED DESCRIPTION - The method, which involves detecting an amplification of unique sequences of at least one position selected from position q24 of human chromosome 8, about position q13 of human chromosome 11 or about position q22-q24 of human chromosome 17 or at least one chromosome arm consisting of the q arm of chromosome 1, 8 or 20 in a genome being tested, comprises:

(a) differentially labeling DNA sequences from the test genome and a normal human genome;

(b) hybridizing the labeled DNA sequences from each of the genomes to a reference genome under the following conditions:

(i) either the labeled DNA sequences or the reference genome, or both, have their repetitive sequences blocked and/or removed;

(ii) DNA unique sequences in the reference genome are retained; and

(c) comparing the intensities of the signals form the labeled DNA sequences as a function of position on the reference genome, therefore allowing detection of the presence or absence of the amplification in the test genome.

USE - CGH is used to determine the relative number of copies of nucleic acid sequences in one or more subject genomes (e.g. DNA of tumor cells) or their portions as a function of the location of those sequences in a reference genome.

ADVANTAGE - CGH determines whether there are abnormal copy numbers of nucleic acid sequences anywhere in the genome of the subject tumor cell or fetal cell without having to prepare condensed chromosome spreads from those cells. CGH also facilitates the genetic analysis of tumors much quicker than prior art methods.

Dwg.0/20

FS CPI

FA AB; DCN

MC CPI: **B04-E01**; B11-C07B3; B11-C08E3; B11-C08E5; **B12-K04F** ; D05-H09; **D05-H18B**

TECH UPTX: 19991124
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The method comprises determining the ratio of the intensities of the signals as a function of position in the reference genome. When detecting amplification of unique sequences, the amplification is detected at position q24 of chromosome 8, about position q13 of human chromosome 11 or about position q22-q24 of human chromosome 17 in the test genome. When detecting amplification of the chromosome arm, the amplification is of the q arm of human chromosome 1, 8 or 20. The reference genome comprises at least one metaphase

chromosome.

ABEX UPTX: 19991124

EXAMPLE - 11 cell lines and 2 primary tumor DNAs were labeled with biotin-14-dATP or digoxigenin-11-dUTP by nick translation. The optimal size for double stranded probe fragments after labeling was 600-1000 bp. Sixty ng of biotinylated test DNA, 60 ng of digoxigeninlabeled normal DNA and 5 ng of unlabeled Cot-1 DNA were ethanol precipitated and dissolved in 10 microl of 50% formamide, 10% dextran sulfate, 2 x SSC, pH 7. The probe mixture was denatured at 70 degrees Centigrade for 5 minutes, allowed to reanneal at 37 degrees Centigrade for 60 minutes and hybridized to normal male metaphase chromosomes for 3-4 days at 37 degrees Centigrade. Immunofluorescent probe detection was carried out at room temperature in three thirty minute steps using 5 microg/mI anti-avidin, 5 microg/ml FITC-avidin and 2 microg/ml anti-digoxigenin-Rhodamine. Nuclei were counterstained with 0.8 microM 4,5-diamino-2-phenylindole (DAPI) in antifade solution. A Zeiss fluorescence microscope equipped with a double band pass filter was used for simultaneous visualization of FITC and rhodamine signals. Analysis of tumor cell lines and primary bladder tumors identified 16 different regions of amplification, many in loci not previously known to be amplified. In 5 of the 11 cell lines, more than one locus was amplified. 2 or 3 separate loci on the same chromosome were amplified in 4 cell lines which suggests a spatial clustering of chromosome locations that undergo DNA amplification.

L25 ANSWER 7 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN 1996-287201 [29] WPIX

DNC C1996-091906

TI Comparing copy number of nucleic acid sequences - by comparative hybridisation of differentially labelled nucleic acids to target elements on a solid support.

DC B04 D16 T01

IN ALBERTSON, D; **GRAY, J W**; PINKEL, D

PA (MEDI-N) MEDICAL RES COUNCIL; (REGC) UNIV CALIFORNIA; (ALBE-I) ALBERTSON D; (GRAY-I) GRAY J W; (PINK-I) PINKEL D

CYC 20

PI WO 9617958 A1 19960613 (199629)* EN 33p C12Q001-68 <--
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: CA JP
EP 800587 A1 19971015 (199746) EN C12Q001-68 <--
R: AT BE CH DE DK ES FR GB IE IT LI NL SE
US 5830645 A 19981103 (199851) C12N001-68
JP 11510681 W 19990921 (199950) 29p C12Q001-68 <--
US 2003008318 A1 20030109 (200311) C12Q001-68 <--
US 6562565 B1 20030513 (200335) C12Q001-68 <--

ADT WO 9617958 A1 WO 1995-US16155 19951208; EP 800587 A1 EP 1995-943084 19951208, WO 1995-US16155 19951208; US 5830645 A US 1994-353018 19941209; JP 11510681 W WO 1995-US16155 19951208, JP 1996-517815 19951208; US 2003008318 A1 Div ex US 1994-353018 19941209, Cont of US 1996-670953 19960626, US 2002-229158 20020828; US 6562565 B1 Cont of US 1994-353018 19941209, US 1996-670953 19960626

FDT EP 800587 A1 Based on WO 9617958; JP 11510681 W Based on WO 9617958; US 2003008318 A1 Div ex US 5830645; US 6562565 B1 Cont of US 5830645

PRAI US 1994-353018 19941209; US 1996-670953 19960626; US 2002-229158 20020828

REP 04Jnl.Ref; US 4981783; US 5028525; US 5194300; US 5447841; WO 9318186

IC ICM C12N001-68; **C12Q001-68**
ICS C07H019-04; C07H021-04; C12N015-09; C12P019-34; G01N033-566; G06K009-40; G06K009-58; G06K009-60; G06T001-00; G06T001-40

AB WO 9617958 A UPAB: 19960724

A method is claimed for comparing copy number of nucleic acid (NA) sequences in collections of 2 NA mols., comprising: (a) providing target elements bound to a solid surface, each target element comprising a target NA, (b) contacting the target elements with: (i) a first collection of

labelled NAs comprising a sequence complementary to a target nucleotide sequence and (ii) 1 second labelled NA comprising a sequence complementary to the target nucleotide sequence, where the first and second labels are distinguishable from each other and (c) detecting the amt. of binding of the first and second labelled complementary NAs to the target NAs.

Also claimed is a kit for quantitating NA sequences in a NA sample, comprising: (a) a solid support having an array of preselected target NAs bound to it, where the array has 2 members, and (b) a container contg. reference NAs which comprise sequences that are complementary and non-complementary to 1 member of the array.

USE - The method is used for comparing abnormal NA copy number and to detect and mapping chromosomal abnormalities associated with diseases such as tumours.

ADVANTAGE - Using the method, the resolution with which copy number change can be mapped is > 10 times better than with standard comparative genomic hybridisation (CGH). This improved localisation facilitates efforts to identify the critical genes involved in a disease and permits more sensitive detection of abnormalities involving a small region of a genome such as in micro-deletion syndromes.

Dwg.0/1

FS CPI EPI

FA AB

MC CPI: B11-C06; B11-C08E5; **B12-K04F**; D05-H09; **D05-H18**
EPI: **T01-J10C4**

L25 ANSWER 8 OF 8 WPIX (C) 2003 THOMSON DERWENT

AN **1993-303497** [38] WPIX

CR 1991-165919 [23]; 1992-217417 [27]; 1992-286380 [35]; 1995-319885 [41]; 1999-037064 [04]; 1999-105095 [09]; 1999-579905 [49]; 1999-619646 [53]; 2001-564345 [63]; 2002-163200 [21]; 2002-303417 [34]; 2003-352179 [33]; 2003-352608 [33]

DNC **C1993-135243**

TI Comparative genomic hybridisation methods - providing in situ detection of amplification(s) and deletions, useful for analysing tumour DNA and for pre-natal diagnosis, e.g. of Downs syndrome.

DC B04 D16

IN **GRAY, J W**; KALLIONIEMI, A; KALLIONIEMI, O P; PINKEL, D; WALDMAN, F; KALLIONIEMI, O; KALLIONIEMI, A P

PA (REGC) UNIV CALIFORNIA

CYC 22

PI

WO 9318186	A1	19930916 (199338)*	EN	88p	C12Q001-68
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP KR					
AU 9337808	A	19931005 (199405)			
EP 631635	A1	19950104 (199506)	EN		
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE					
JP 07505053	W	19950608 (199531)			C12Q001-68
US 5665549	A	19970909 (199742)		42p	C12Q001-68
US 5721098	A	19980224 (199815)		42p	C12Q001-68
US 6159685	A	20001212 (200067)			C12Q001-68
EP 631635	B1	20010912 (200155)	EN		C12Q001-68
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE					
EP 1134293	A2	20010919 (200155)	EN		C12Q001-68
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE					
DE 69330750	E	20011018 (200169)			C12Q001-68
ES 2161715	T3	20011216 (200206)			C12Q001-68
CA 2131543	C	20020917 (200267)	EN		C12Q001-68
CA 2392673	A1	19930916 (200271)	EN		C12Q001-68

ADT WO 9318186 A1 WO 1993-US1775 19930301; AU 9337808 A AU 1993-37808 19930301; EP 631635 A1 EP 1993-907077 19930301, WO 1993-US1775 19930301; JP 07505053 W JP 1993-515791 19930301, WO 1993-US1775 19930301; US 5665549 A CIP of US 1992-846659 19920304, Cont of US 1992-969948 19921030, Div ex

US 1993-166147 19931214, US 1995-466122 19950606; US 5721098 A CIP of US 1986-819314 19860116, CIP of US 1986-937793 19861204, CIP of US 1989-444669 19891201, CIP of US 1990-497098 19900320, CIP of US 1990-537305 19900612, CIP of US 1991-659974 19910222, CIP of US 1991-670242 19910315, CIP of US 1992-846659 19920304, Cont of US 1992-969948 19921030, Cont of US 1993-166147 19931214, US 1995-468629 19950606; US 6159685 A CIP of US 1986-819314 19860116, CIP of US 1986-937793 19861204, CIP of US 1989-444669 19891201, CIP of US 1990-497098 19900320, CIP of US 1990-537305 19900612, Cont of US 1990-627707 19901214, CIP of US 1991-659974 19910222, CIP of US 1991-670242 19910315, CIP of US 1992-846659 19920304, Cont of US 1992-969948 19921030, Cont of US 1993-166147 19931214, Cont of US 1995-468629 19950606, US 1997-903095 19970730; EP 631635 B1 EP 1993-907077 19930301, WO 1993-US1775 19930301, Related to EP 2001-200109 19930301; EP 1134293 A2 Div ex EP 1993-907077 19930301, EP 2001-200109 19930301; DE 69330750 E DE 1993-630750 19930301, EP 1993-907077 19930301, WO 1993-US1775 19930301; ES 2161715 T3 EP 1993-907077 19930301; CA 2131543 C CA 1993-2131543 19930301, WO 1993-US1775 19930301; CA 2392673 A1 Div ex CA 1993-2131543 19930301, CA 1993-2392673 19930301

FDT AU 9337808 A Based on WO 9318186; EP 631635 A1 Based on WO 9318186; JP 07505053 W Based on WO 9318186; US 6159685 A Cont of US 5447841, Cont of US 5721098; EP 631635 B1 Based on WO 9318186; EP 1134293 A2 Div ex EP 631635; DE 69330750 E Based on EP 631635, Based on WO 9318186; ES 2161715 T3 Based on EP 631635; CA 2131543 C Based on WO 9318186

PRAI US 1992-969948 19921030; US 1992-846659 19920304; US 1993-166147 19931214; US 1995-466122 19950606; US 1986-819314 19860116; US 1986-937793 19861204; US 1989-444669 19891201; US 1990-497098 19900320; US 1990-537305 19900612; US 1991-659974 19910222; US 1991-670242 19910315; US 1995-468629 19950606; US 1990-627707 19901214; US 1997-903095 19970730

REP 3.Jnl.Ref; EP 430402; WO 9005789

IC ICM C12Q001-68
ICS C07H021-02; C07H021-04; C12N015-09; C12P011-34; C12P019-34

AB WO 9318186 A UPAB: 20030526
Comparing copy numbers of different DNA sequences in a subject cell or cell population comprises: (a) extracting the DNA from the subject cell or from a number of cells of the subject cell population; (b) amplifying the extd. DNA, if necessary; (c) labelling the DNA; (d) hybridising the labelled DNA in situ to reference metaphase chromosomes, after removing from the labelled DNA, those repetitive sequences which could bind to multiple loci in the reference metaphase chromosomes, and/or after blocking the binding sites for those repetitive sequences in the reference metaphase chromosomes by pre-hybridisation with appropriate blocking nucleic acids, and/or blocking those repetitive sequences in the labelled subject DNA by pre-hybridisation with appropriate blocking nucleic acid sequences; (e) rendering the bound, labelled DNA sequences, visualisable, if necessary; (f) observing and/or measuring the intensity of the signal from the bound labelled DNA sequences as a function of position on the reference metaphase chromosomes; and (g) comparing the copy numbers of different DNA sequences of the subject DNA by comparing the signal intensities at different positions on the reference metaphase chromosomes, where the greater the signal intensity at a given position, the greater the copy number of the sequences in the subejct DNA which bind at that position.

USE/ADVANTAGE - The comparative genomic hybridisation (CGH) methods can be qualitative or quantitative and are partic. useful for analysing DNA sequences from cells from clinical specimens including tumour and foetal tissue. CGH may be used to detect sequence copy number inbalances throughout an entire genome in one hybridisation, to map gains and/or losses of sequences in a genome and/or to provide a copy number karyotype of a subject genome. Specific applications include early detection of amplifications and/or deletions in cells from a suspected lesion and prenatal detection of an extra copy of chromosome 21, diagnostic of Down's

Syndrome
Dwg.0/9
FS CPI
FA AB
MC CPI: **B04-B04A1**; B11-C08E; B12-K04A3; **D05-H12**
ABEQ US 5665549 A UPAB: 19971021
A method of comparing copy numbers of unique DNA sequences in a first cell or cell population relative to copy numbers of substantially identical sequences in a second cell or cell population, said method comprising the steps of:
(a) labelling genomic DNA sequences from each cell or cell population with a different label;
(b) hybridizing said labelled DNA sequences from each cell or cell population to a reference genome under the following conditions:
(i) either the labelled DNA sequences, and/or the reference genome have their repetitive sequences blocked and/or removed; and
(ii) unique DNA sequences in the labelled DNA sequences and unique DNA sequences in the reference genome are retained;
(c) comparing the intensities of the signals from the labelled DNA sequences hybridized to the reference genome.
Dwg.0/13
ABEQ US 5721098 A UPAB: 19980410
Comparing copy numbers of different DNA sequences in a subject cell or cell population comprises: (a) extracting the DNA from the subject cell or from a number of cells of the subject cell population; (b) amplifying the extd. DNA, if necessary; (c) labelling the DNA; (d) hybridising the labelled DNA in situ to reference metaphase chromosomes, after removing from the labelled DNA, those repetitive sequences which could bind to multiple loci in the reference metaphase chromosomes, and/or after blocking the binding sites for those repetitive sequences in the reference metaphase chromosomes by pre-hybridisation with appropriate blocking nucleic acids, and/or blocking those repetitive sequences in the labelled subject DNA by pre-hybridisation with appropriate blocking nucleic acid sequences; (e) rendering the bound, labelled DNA sequences, visualisable, if necessary; (f) observing and/or measuring the intensity of the signal from the bound labelled DNA sequences as a function of position on the reference metaphase chromosomes; and (g) comparing the copy numbers of different DNA sequences of the subject DNA by comparing the signal intensities at different positions on the reference metaphase chromosomes, where the greater the signal intensity at a given position, the greater the copy number of the sequences in the subejct DNA which bind at that position.
USE/ADVANTAGE - The comparative genomic hybridisation (CGH) methods can be qualitative or quantitative and are partic. useful for analysing DNA sequences from cells from clinical specimens including tumour and foetal tissue. CGH may be used to detect sequence copy number inbalances throughout an entire genome in one hybridisation, to map gains and/or losses of sequences in a genome and/or to provide a copy number karyotype of a subject genome. Specific applications include early detection of amplifications and/or deletions in cells from a suspected lesion and prenatal detection of an extra copy of chromosome 21, diagnostic of Down's Syndrome
Dwg.0/13

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FILE LAST UPDATED: 14 JUL 2003 <20030714/UP>
PATENTS CITATION INDEX, COVERS 1973 TO DATE

>>> LEARNING FILE LDPCI AVAILABLE <<<

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L26  ANSWER 1 OF 1  DPCI  COPYRIGHT 2003 THOMSON DERWENT
AN   2002-114358 [15]   DPCI
DNC  C2002-035107
TI   New method of comparing test and reference genome in identifying
     rearrangement in tumor genomes comprising sequencing the ends of obtained
     inserts from the test genome and comparing the co-linearity of the ends
     with corresponding sequences.
DC   B04 D16
IN   COLLINS, C; GRAY, J W; VOLIK, S
PA   (REGC) UNIV CALIFORNIA
CYC  96
PI   WO 2001092558 A2 20011206 (200215)* EN   38p    C12Q000-00       <--
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            KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU
            SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
     AU 2001075110 A  20011211 (200225)              C12Q000-00
ADT  WO 2001092558 A2 WO 2001-US17757 20010531; AU 2001075110 A AU 2001-75110
     20010531
FDT  AU 2001075110 A Based on WO 200192558
PRAI US 2000-586529   20000531
IC   ICM  C12Q000-00
FS   CPI

CTCS CITATION COUNTERS
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PNC.DI    0              Cited Patents Count (by inventor)
PNC.DX    2              Cited Patents Count (by examiner)
IAC.DI    0              Cited Issuing Authority Count (by inventor)
IAC.DX    1              Cited Issuing Authority Count (by examiner)

PNC.GI    0              Citing Patents Count (by inventor)
PNC.GX    0              Citing Patents Count (by examiner)
IAC.GI    0              Citing Issuing Authority Count (by inventor)
IAC.GX    0              Citing Issuing Authority Count (by examiner)

CRC.I     0              Cited Literature References Count (by inventor)
CRC.X     1              Cited Literature References Count (by examiner)

CDP  CITED PATENTS       UPD: 20030709
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     Cited by Examiner
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     CITING PATENT    CAT    CITED PATENT     ACCNO
     ------------------------------------------------------
     WO 200192558  A  X      US 5830645    A  1996-287201/29
                    PA:  (MEDI-N) MEDICAL RES COUNCIL; (REGC) UNIV CALIFORNIA;
                         (ALBE-I) ALBERTSON D; (GRAY-I) GRAY J W; (PINK-I)
                         PINKEL D
                    IN:  ALBERTSON, D; GRAY, J W; PINKEL, D
                      X      US 6013439    A  1997-351081/32
                    PA:  (BEHW) BEHRINGWERKE AG; (ULLM-I) ULLMAN E; (ULLM-I)
                         ULLMAN E F; (KURN-I) KURN N; (LISH-I) LISHANSKI A;
                         (DADE-N) DADE BEHRING MARBURG GMBH
                    IN:  KURN, N; LISHANSKI, A; ULLMAN, E F
```

REN LITERATURE CITATIONS UPR: 20030709

Citations by Examiner

CITING PATENT	CAT	CITED LITERATURE
WO 200192558	A	ALTSCHUL S.F. ET AL.: 'Basic local alignment tool' J. MOL. BIOL. vol. 215, 05 October 1990, pages 403 - 410, XP002949123

=> fil wpix
FILE 'WPIX' ENTERED AT 14:11:35 ON 16 JUL 2003

FILE LAST UPDATED: 10 JUL 2003 <20030710/UP>
MOST RECENT DERWENT UPDATE: 200344 <200344/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

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>>> SLART (Simultaneous Left and Right Truncation) is now available in the /ABEX field. An additional search field /BIX is also provided which comprises both /BI and /ABEX <<<

>>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

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http://www.derwent.com/userguides/dwpi_guide.html <<<

=> d all abeq tech abex

L28 ANSWER 1 OF 1 WPIX (C) 2003 THOMSON DERWENT
AN 1997-351081 [32] WPIX
DNN N1997-290911 DNC C1997-113482
TI Detection of differences in related nucleic acids - comprises forming a complex of the DNA and detecting the presence of the complex.
DC B04 D16 S03
IN KURN, N; LISHANSKI, A; ULLMAN, E F
PA (BEHW) BEHRINGWERKE AG; (ULLM-I) ULLMAN E; (ULLM-I) ULLMAN E F; (KURN-I) KURN N; (LISH-I) LISHANSKI A; (DADE-N) DADE BEHRING MARBURG GMBH
CYC 23
PI WO 9723646 A1 19970703 (199732)* EN 96p C12Q001-68
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: AU CA JP KR MX
AU 9715653 A 19970717 (199745) C12Q001-68
EP 920532 A1 19990609 (199927) EN C12Q001-68
R: AT BE DE FR GB IT NL
US 6013439 A 20000111 (200010) C12Q001-68 <--
US 2001014450 A1 20010816 (200149) C12Q001-68
US 6555317 B2 20030429 (200331) C12Q001-68
ADT WO 9723646 A1 WO 1996-US19750 19961220; AU 9715653 A AU 1997-15653 19961220; EP 920532 A1 EP 1996-945386 19961220, WO 1996-US19750 19961220;

US 6013439 A Provisional US 1995-9289P 19951222, Provisional US 1996-12929P 19960306, US 1996-771623 19961220; US 2001014450 A1 Provisional US 1995-9289P 19951222, Provisional US 1996-12929P 19960306, Cont of US 1996-771623 19961220, Cont of US 1999-370919 19990809, US 2000-732279 20001207; US 6555317 B2 Provisional US 1995-9289P 19951222, Provisional US 1996-12929P 19960306, Cont of US 1996-771623 19961220, Cont of US 1999-370919 19990809, US 2000-732279 20001207

FDT AU 9715653 A Based on WO 9723646; EP 920532 A1 Based on WO 9723646; US 2001014450 A1 Cont of US 6013439; US 6555317 B2 Cont of US 6013439

PRAI US 1996-12929P 19960306; US 1995-9289P 19951222; US 1996-771623 19961220; US 1999-370919 19990809; US 2000-732279 20001207

REP 3.Jnl.Ref; EP 450370; EP 469755; WO 9403812

IC ICM C12Q001-68
ICS C07H021-00; C07H021-02; C12P019-34; G01N033-58

AB WO 9723646 A UPAB: 19970806
Methods for the detection of differences in related nucleic acid sequences are claimed.

USE - The methods provide detection of any differences in two related nucleic acid sequences, whether differences are known or not. These methods are simple, inexpensive and sensitive for detecting mutations, and are suitable for large scale population screenings.

Dwg.0/9

FS CPI EPI

FA AB

MC CPI: B04-E01; B11-C08E3; B12-K04F; D05-H09
EPI: S03-E14H9

=> fil medline
FILE 'MEDLINE' ENTERED AT 14:12:55 ON 16 JUL 2003

FILE LAST UPDATED: 15 JUL 2003 (20030715/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/changes2003.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all

L29 ANSWER 1 OF 1 MEDLINE

AN 91039304 MEDLINE

DN 91039304 PubMed ID: 2231712

TI Basic local alignment search tool.

AU **Altschul S F**; Gish W; Miller W; Myers E W; Lipman D J

CS National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894.

NC LM04960 (NLM)
LM05110 (NLM)

SO JOURNAL OF MOLECULAR BIOLOGY, **(1990 Oct 5) 215** (3) **403-10.**
Journal code: 2985088R. ISSN: 0022-2836.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199012

ED Entered STN: 19910208
Last Updated on STN: 19910208

Entered Medline: 19901205

AB A new approach to rapid sequence comparison, basic local alignment search tool (BLAST), directly approximates alignments that optimize a measure of local similarity, the maximal segment pair (MSP) score. Recent mathematical results on the stochastic properties of MSP scores allow an analysis of the performance of this method as well as the statistical significance of alignments it generates. The basic algorithm is simple and robust; it can be implemented in a number of ways and applied in a variety of contexts including straightforward DNA and protein sequence database searches, motif searches, gene identification searches, and in the analysis of multiple regions of similarity in long DNA sequences. In addition to its flexibility and tractability to mathematical analysis, BLAST is an order of magnitude faster than existing sequence comparison tools of comparable sensitivity.

CT Check Tags: Support, U.S. Gov't, P.H.S.
Algorithms
Amino Acid Sequence
*Base Sequence
Databases, Factual
*Mutation
Sensitivity and Specificity
Sequence Homology, Nucleic Acid
*Software

=> fil medline
FILE 'MEDLINE' ENTERED AT 16:21:59 ON 15 JUL 2003

FILE LAST UPDATED: 13 JUL 2003 (20030713/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/changes2003.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all tot

L64 ANSWER 1 OF 10 MEDLINE
AN 2003297305 IN-PROCESS
DN 22709111 PubMed ID: 12788976
TI **End-sequence profiling**: sequence-based analysis of aberrant **genomes**.
AU **Volik Stanislav**; Zhao Shaying; Chin Koei; Brebner John H; Herndon David R; Tao Quanzhou; Kowbel David; Huang Guiqing; Lapuk Anna; Kuo Wen-Lin; Magrane Gregg; De Jong Pieter; **Gray Joe W**; **Collins Colin**
CS Cancer Research Institute and Department of Laboratory Medicine, University of California Comprehensive Cancer Center, 2340 Sutter Street, San Francisco, CA 94115, USA.
NC CA58207 (NCI)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2003 Jun 24) 100 (13) 7696-701.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
OS GENBANK-BZ597614; GENBANK-BZ597615; GENBANK-BZ597616; GENBANK-BZ597617;
GENBANK-BZ597618; GENBANK-BZ597619; GENBANK-BZ597620; GENBANK-BZ597621;
GENBANK-BZ597622; GENBANK-BZ597623; GENBANK-BZ597624; GENBANK-BZ597625;
GENBANK-BZ597626; GENBANK-BZ597627; GENBANK-BZ597628; GENBANK-BZ597629;
GENBANK-BZ597630; GENBANK-BZ597631; GENBANK-BZ597632; GENBANK-BZ597633;
GENBANK-BZ597634; GENBANK-BZ597635; GENBANK-BZ597636; GENBANK-BZ597637;
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GENBANK-BZ597642; GENBANK-BZ597643; GENBANK-BZ597644; GENBANK-BZ597645;
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GENBANK-BZ598478; GENBANK-BZ598479; GENBANK-BZ598480; GENBANK-BZ598481;
GENBANK-BZ598482; GENBANK-BZ598483; GENBANK-BZ598484; GENBANK-BZ598485;
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GENBANK-BZ598518; GENBANK-BZ598519; GENBANK-BZ598520; GENBANK-BZ598521;
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GENBANK-BZ598586; GENBANK-BZ598587; GENBANK-BZ598588; GENBANK-BZ598589;
GENBANK-BZ598590; GENBANK-BZ598591; GENBANK-BZ598592; GENBANK-BZ598593;
GENBANK-BZ598594; GENBANK-BZ598595; GENBANK-BZ598596; GENBANK-BZ598597;
GENBANK-BZ598598; GENBANK-BZ598599; GENBANK-BZ598600; GENBANK-BZ598601;
GENBANK-BZ598602; GENBANK-BZ598603; GENBANK-BZ598604; GENBANK-BZ598605;
GENBANK-BZ598606; GENBANK-BZ598607; GENBANK-BZ598608; GENBANK-BZ598609;
GENBANK-BZ598610; GENBANK-BZ598611; GENBANK-BZ598612; GENBANK-BZ598613

ED Entered STN: 20030626
Last Updated on STN: 20030709

AB **Genome** rearrangements are important in evolution, cancer, and other diseases. Precise mapping of the rearrangements is essential for identification of the involved genes, and many techniques have been developed for this purpose. We show here that **end-sequence profiling** (**ESP**) is particularly well suited to this purpose. **ESP** is accomplished by constructing a bacterial artificial **chromosome** (BAC) library from a test **genome**, measuring BAC **end sequences**, and mapping **end-sequence** pairs onto the normal **genome** sequence. Plots of BAC **end-sequences** density identify copy number abnormalities at high resolution. BACs spanning structural aberrations have end pairs that map abnormally far apart on the normal **genome** sequence. These pairs can then be sequenced to determine the involved genes and breakpoint sequences. **ESP** analysis of the breast cancer cell line MCF-7 demonstrated its utility for analysis of complex **genomes**. **End sequencing** of approximately 8,000 **clones** (0.37-fold haploid **genome clonal** coverage) produced a comprehensive **genome** copy number map of the MCF-7 **genome** at better than 300-kb resolution and identified 381 **genome** breakpoints, a subset of which was verified by fluorescence in situ hybridization mapping and sequencing.

L64 ANSWER 2 OF 10 MEDLINE
AN **2001105556** MEDLINE
DN **20568493** PubMed ID: **11116098**
TI Detection of deleted **genomic DNA** using a semiautomated

computational analysis of GeneChip data.
CM Comment in: Genome Res. 2000 Dec;10(12):1837-9
AU Salamon H; Kato-Maeda M; Small P M; Drenkow J; Gingeras T R
CS Division of Infectious Diseases and Geographic Medicine, Department of Medicine, Stanford University, Stanford, California 94305, USA.. Hugh_Salamon@Berlex.com
SO GENOME RESEARCH, **(2000 Dec)** 10 (12) 2044-54.
Journal code: 9518021. ISSN: 1088-9051.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010208
AB **Genomic** diversity within and between populations is caused by single nucleotide mutations, changes in repetitive **DNA** systems, recombination mechanisms, and insertion and deletion events. The contribution of these sources to diversity, whether purely genetic or of phenotypic consequence, can only be investigated if we have the means to quantitate and characterize diversity in many samples. With the advent of complete sequence characterization of representative **genomes** of different species, the possibility of developing protocols to screen for genetic polymorphism across entire **genomes** is actively being pursued. The large numbers of measurements such approaches yield demand that we pay careful attention to the numerical analysis of data. In this paper we present a novel application of an Affymetrix GeneChip to perform **genome**-wide screens for deletion polymorphism. A high-density oligonucleotide array formatted for mRNA expression and targeted at a fully sequenced 4.4-million-base pair Mycobacterium tuberculosis standard strain **genome** was adapted to compare **genomic** **DNA**. Hybridization intensities to 111,000 probe pairs (perfect complement and mismatch complement) were measured for **genomic** **DNA** from a clinical strain and from a vaccine organism. Because individual probe-pair hybridization intensities exhibit limited sensitivity/specificity characteristics to detect deletions, data-analytical methodology to exploit measurements from multiple probes in tandem locations across the **genome** was developed. The TSTEP (Tandem Set **Terminal** Extreme Probability) algorithm designed specifically to analyze the tandem hybridization measurements data was applied and shown to discover **genomic** deletions with high sensitivity. The TSTEP algorithm provides a foundation for similar efforts to characterize deletions in many hybridization measures in similar-sized and larger **genomes**. Issues relating to the design of **genome** content screening experiments and the implications of these methods for studying population **genomics** and the evolution of **genomes** are discussed.
CT Algorithms
***Computational Biology: MT, methods**
***DNA, Bacterial: AN, analysis**
***DNA, Bacterial: GE, genetics**
Genes, Bacterial: GE, genetics
Genome, Bacterial
Mycobacterium bovis: GE, genetics
Mycobacterium tuberculosis: GE, genetics
***Oligonucleotide Array Sequence Analysis: MT, methods**
*Sequence Deletion: GE, genetics
CN 0 (**DNA**, Bacterial)

L64 ANSWER 3 OF 10 MEDLINE
AN **2000433824** MEDLINE
DN **20277483** PubMed ID: **10819332**

CS Laboratory for Computer Science, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139 USA.
SO GENOME RESEARCH, **(1999 Dec)** 9 (12) 1163-74.
Journal code: 9518021. ISSN: 1088-9051.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200001
ED Entered STN: 20000204
Last Updated on STN: 20000204
Entered Medline: 20000127
AB One approach to sequencing a large **genome** is (1) to sequence a collection of nonoverlapping "seeds" chosen from a **genomic** library of large-insert **clones** [such as bacterial artificial **chromosomes** (BACs)] and then (2) to take successive "walking" steps by selecting and sequencing minimally overlapping **clones**, using information such as **clone-end sequences** to identify the overlaps. In this paper we analyze the strategic issues involved in using this approach. We derive formulas showing how two key factors, the initial density of seed **clones** and the depth of the **genomic** library used for walking, affect the cost and time of a sequencing project-that is, the amount of redundant sequencing and the number of steps to cover the vast majority of the **genome**. We also discuss a variant strategy in which a second **genomic** library with **clones** having a somewhat smaller insert size is used to close gaps. This approach can dramatically decrease the amount of redundant sequencing, without affecting the rate at which the **genome** is covered.
CT Check Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
***Chromosome Walking: MT, methods**
Chromosomes, Bacterial
Cloning, Molecular: MT, methods
***Genome**
Models, Genetic
***Sequence Analysis, DNA: MT, methods**

L64 ANSWER 6 OF 10 MEDLINE
AN **1999157099** MEDLINE
DN **99157099** PubMed ID: **10037818**
TI High throughput direct **end sequencing** of BAC **clones**.
AU Kelley J M; Field C E; Craven M B; Bocskai D; Kim U J; Rounsley S D; Adams M D
CS The Institute for Genomic Research, Rockville, MD 20850, USA and Division of Biology,California Institute of Technology, Pasadena, CA 91125, USA.
SO NUCLEIC ACIDS RESEARCH, **(1999 Mar 15)** 27 (6) 1539-46.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199904
ED Entered STN: 19990511
Last Updated on STN: 19990511
Entered Medline: 19990427
AB Libraries constructed in bacterial artificial **chromosome** (BAC) vectors have become the choice for **clone** sets in high throughput **genomic** sequencing projects primarily because of their high stability. BAC libraries have been proposed as a source for minimally over-lapping **clones** for sequencing large **genomic** regions, and the use of BAC **end sequences** (i.e. sequences adjoining the insert sites) has been proposed as a primary means

for selecting minimally overlapping **clones** for sequencing large **genomic** regions. For this strategy to be effective, high throughput methods for BAC **end sequencing** of all the **clones** in deep coverage BAC libraries needed to be developed. Here we describe a low cost, efficient, 96 well procedure for BAC **end sequencing**. These methods allow us to generate BAC **end sequences** from human and Arabidoposis libraries with an average read length of >450 bases and with a single pass sequencing average accuracy of >98%. Application of BAC **end sequences** in **genomic** sequen-cing is discussed.

CT Check Tags: Human; Support, U.S. Gov't, Non-P.H.S.
Arabidopsis: GE, genetics
Base Sequence
***Chromosomes, Bacterial**
Cloning, Molecular: MT, methods
*F Factor
Gene Library
Molecular Sequence Data
Selection (Genetics)
Sequence Analysis, DNA: EC, economics
***Sequence Analysis, DNA: MT, methods**

CN 0 (F Factor)

L64 ANSWER 7 OF 10 MEDLINE
AN **97264341** MEDLINE
DN **97264341** PubMed ID: **9110174**
TI Large-scale concatenation cDNA sequencing.
AU Yu W; Andersson B; Worley K C; Muzny D M; Ding Y; Liu W; Ricafrente J Y; Wentland M A; Lennon G; Gibbs R A
NC 1F32 HG00169-01 (NHGRI)
P30 HG00210-05 (NHGRI)
R01 HG00823 (NHGRI)
SO GENOME RESEARCH, **(1997 Apr)** 7 (4) 353-8.
Journal code: 9518021. ISSN: 1088-9051.
CY United States
DT Letter
LA English
FS Priority Journals
OS GENBANK-AF007128; GENBANK-AF007129; GENBANK-AF007130; GENBANK-AF007131; GENBANK-AF007132; GENBANK-AF007133; GENBANK-AF007134; GENBANK-AF007135; GENBANK-AF007136; GENBANK-AF007137; GENBANK-AF007138; GENBANK-AF007139; GENBANK-AF007140; GENBANK-AF007141; GENBANK-AF007142; GENBANK-AF007143; GENBANK-AF007144; GENBANK-AF007145; GENBANK-AF007146; GENBANK-AF007147; GENBANK-AF007148; GENBANK-AF007149; GENBANK-AF007150; GENBANK-AF007151; GENBANK-AF007152; GENBANK-AF007153; GENBANK-AF007154
EM 199706
ED Entered STN: 19970630
Last Updated on STN: 20000303
Entered Medline: 19970617
AB A total of 100 kb of **DNA** derived from 69 individual human brain cDNA **clones** of 0.7-2.0 kb were sequenced by concatenated cDNA sequencing (CCS), whereby multiple individual **DNA** fragments are sequenced simultaneously in a single shotgun library. The method yielded accurate sequences and a similar efficiency compared with other shotgun libraries constructed from single **DNA** fragments (> 20 kb). Computer analyses were carried out on 65 cDNA **clone** sequences and their corresponding **end sequences** to examine both nucleic acid and amino acid sequence similarities in the databases. Thirty-seven **clones** revealed no **DNA** database matches, 12 **clones** generated exact matches (> or = 98% identity), and 16 **clones** generated nonexact matches (57%-97% identity) to either known human or other species genes. Of those 28 matched **clones**, 8 had corresponding **end sequences** that failed to

identify similarities. In a protein similarity search, 27 **clone** sequences displayed significant matches, whereas only 20 of the **end sequences** had matches to known protein sequences. Our data indicate that full-length cDNA insert sequences provide significantly more nucleic acid and protein sequence similarity matches than expressed sequence tags (ESTs) for database searching.

CT Check Tags: Human; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
DNA Transposable Elements
DNA, Complementary: CH, chemistry
***DNA, Complementary: GE, genetics**
Databases, Factual
Gene Library
Molecular Sequence Data
Proteins: CH, chemistry
*Proteins: GE, genetics
***Sequence Alignment: MT, methods**
***Sequence Analysis, DNA: MT, methods**
Sequence Homology, Amino Acid
Sequence Homology, Nucleic Acid
Software

CN 0 (**DNA** Transposable Elements); 0 (**DNA**, Complementary); 0 (Proteins)

L64 ANSWER 8 OF 10 MEDLINE

AN **97092874** MEDLINE

DN **97092874** PubMed ID: **8938436**

TI **End sequence** determination from large insert **clones** using energy transfer fluorescent primers.

AU Marra M; Weinstock L A; Mardis E R

CS Genome Sequencing Center, St. Louis, Missouri 63108, USA.

SO GENOME RESEARCH, **(1996 Nov)** 6 (11) 1118-22.
Journal code: 9518021. ISSN: 1088-9051.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199702

ED Entered STN: 19970306
Last Updated on STN: 19980206
Entered Medline: 19970227

AB **Genome** mapping strategies depend heavily on confirmatory data of several types to establish overlaps between contiguous stretches of **cloned DNA** derived from **genomic** regions. One type of ancillary data that can contribute to establishing these overlaps is **DNA** sequence data derived from the ends of large (> 30 kb) inserts in **genomic clones**. This type of data can be difficult to obtain routinely, because large **clones** are often unstable and microgram quantities of highly purified **DNA** are required in each sequencing reaction to obtain sufficient signal for accurate base calling and maximum read length. Recently, we have been experimenting with methods to consistently obtain up to 800 bases of high-quality sequence data from the ends of large insert **clones** using ThermoSequenase **DNA** polymerase and Energy Transfer fluorescent primers. Our experimental approach and results, described in this paper, indicate that routinely obtaining high-quality sequence data from the ends of large insert **genomic clones** is feasible. Such data can contribute to the assessment of common regions between large insert **clones**, to the establishment of conservation of synteny between closely related species, and to the detection of additional contiguous **clones**.

CT ***Chromosome Mapping: MT, methods**
Cloning, Molecular

DNA: AN, analysis
DNA Primers: CH, chemistry
DNA Primers: GE, genetics
DNA-Directed DNA Polymerase: ME, metabolism
Fluorescence
***Sequence Analysis: MT, methods**
RN **9007-49-2 (DNA)**
CN 0 (**DNA** Primers); EC 2.7.7.7 (**DNA**-Directed **DNA** Polymerase)

L64 ANSWER 9 OF 10 MEDLINE
AN 96121589 MEDLINE
DN 96121589 PubMed ID: 8595414
TI Quantitative **DNA** fiber mapping.
AU Weier H U; Wang M; Mullikin J C; Zhu Y; Cheng J F; Greulich K M; Bensimon A; **Gray J W**
CS Center for Molecular Cytogenetics, University of California, Lawrence Berkeley Laboratory, Berkeley 94720, USA.
NC CA 58207 (NCI)
SO HUMAN MOLECULAR GENETICS, **(1995 Oct)** 4 (10) 1903-10.
Journal code: 9208958. ISSN: 0964-6906.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U09128; GENBANK-X54156; GENBANK-X65279
EM 199604
ED Entered STN: 19960424
Last Updated on STN: 19960424
Entered Medline: 19960418
AB The assembly of sequence ready, high-resolution physical maps and construction of minimally overlapping contigs for the human as well as model **genomes** requires accurate determination of the extent of overlap between adjacent **clones** as well as their relative orientation. This is presently done by procedures such as **clone** fingerprinting, Southern blot analysis or **clone end sequencing**. We present a complementary analytical technique to map directly **cloned DNA** sequences on to individual stretched **DNA** molecules. This approach uses the hydrodynamic force of a receding meniscus to prepare straight high molecular weight **DNA** molecules that provide a linear template of approximately 2.3 kb/microns on to which the **cloned** probes can be mapped by in situ hybridization. This technique has numerous advantages such as a very high density of mapping templates, reproducible stretching of the mapping template providing a linear **genomic** scale, determination of **clone** orientation and direct visualization of **DNA** repeats. The utility and accuracy of quantitative **DNA** fiber mapping are illustrated through three examples: (i) mapping of lambda **DNA** restriction fragments along linearized approximately 49 kb long lambda phage **DNA** molecules with approximately 1 kb precision; (ii) localization of the overlap between a cosmid and a colinear P1 **clone**; and (iii) mapping of P1 **clones** along an approximately 490 kb yeast artificial **chromosome** (YAC) with approximately 5 kb precision and estimation of the approximately 25 kb gap between them.
CT Check Tags: Human; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Bacteriophage lambda: GE, genetics
***Chromosome Mapping**
Chromosomes, Artificial, Yeast
Cloning, Molecular
Cosmids
DNA: CH, chemistry

DNA: GE, genetics
DNA Probes
DNA, Viral: CH, chemistry
DNA, Viral: GE, genetics
***Genome**
***Genome, Human**
In Situ Hybridization, Fluorescence
Molecular Sequence Data
Restriction Mapping
RN **9007-49-2 (DNA)**
CN 0 (**Chromosomes**, Artificial, Yeast); 0 (Cosmids); 0 (**DNA** Probes); 0 (**DNA**, Viral)

L64 ANSWER 10 OF 10 MEDLINE
AN **95324927** MEDLINE
DN **95324927** PubMed ID: **7601461**
TI Pairwise **end sequencing**: a unified approach to **genomic** mapping and sequencing.
AU Roach J C; Boysen C; Wang K; Hood L
CS Department of Molecular Biotechnology, University of Washington, Seattle 98195, USA.
SO GENOMICS, **(1995 Mar 20)** 26 (2) 345-53.
Journal code: 8800135. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950822
Last Updated on STN: 19950822
Entered Medline: 19950808
AB Strategies for large-scale **genomic DNA** sequencing currently require physical mapping, followed by detailed mapping, and finally sequencing. The level of mapping detail determines the amount of effort, or sequence redundancy, required to finish a project. Current strategies attempt to find a balance between mapping and sequencing efforts. One such approach is to employ strategies that use sequence data to build physical maps. Such maps alleviate the need for prior mapping and reduce the final required sequence redundancy. To this end, the utility of correlating pairs of sequence data derived from both ends of subcloned templates is well recognized. However, optimal strategies employing such pairwise data have not been established. In the present work, we simulate and analyze the parameters of pairwise sequencing projects including template length, sequence read length, and total sequence redundancy. One pairwise strategy based on sequencing both ends of plasmid subclones is recommended and illustrated with raw data simulations. We find that pairwise strategies are effective with both small (cosmid) and large (megaYAC) targets and produce ordered sequence data with a high level of mapping completeness. They are ideal for finescale mapping and gene finding and as initial steps for either a high- or a low-redundancy sequencing effort. Such strategies are highly automatable.
CT Check Tags: Support, Non-U.S. Gov't
Base Composition
***Chromosome Mapping: MT, methods**
Computer Simulation
Cosmids: GE, genetics
***Genome**
***Sequence Analysis, DNA: MT, methods**
Templates, Genetic
CN 0 (Cosmids)

not for comparison. But clearly delineated advantages may include in mapping reg.

=> fil medline
FILE 'MEDLINE' ENTERED AT 14:40:14 ON 16 JUL 2003

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all tot

L66 ANSWER 1 OF 3 MEDLINE
AN **1999157099** MEDLINE
DN **99157099** PubMed ID: **10037818**
TI High throughput direct **end sequencing** of BAC clones.
AU Kelley J M; Field C E; Craven M B; Bocskai D; Kim U J; Rounsley S D; Adams M D
CS The Institute for Genomic Research, Rockville, MD 20850, USA and Division of Biology,California Institute of Technology, Pasadena, CA 91125, USA.
SO NUCLEIC ACIDS RESEARCH, **(1999 Mar 15)** 27 (6) 1539-46.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom .
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199904
ED Entered STN: 19990511
Last Updated on STN: 19990511
Entered Medline: 19990427
AB Libraries constructed in bacterial artificial chromosome (BAC) vectors have become the choice for clone sets in high throughput genomic sequencing projects primarily because of their high stability. BAC libraries have been proposed as a source for minimally over-lapping clones for sequencing large genomic regions, and the use of BAC **end sequences** (i.e. sequences adjoining the insert sites) has been proposed as a primary means for selecting minimally overlapping clones for sequencing large genomic regions. For this strategy to be effective, high throughput methods for BAC **end sequencing** of all the clones in deep coverage BAC libraries needed to be developed. Here we describe a low cost, efficient, 96 well procedure for BAC **end sequencing**. These methods allow us to generate BAC **end sequences** from human and Arabidopsis libraries with an average read length of >450 bases and with a single pass sequencing average accuracy of >98%. Application of BAC **end sequences** in genomic sequen-cing is discussed.
CT Check Tags: Human; Support, U.S. Gov't, Non-P.H.S.
Arabidopsis: GE, genetics
Base Sequence
***Chromosomes, Bacterial**
Cloning, Molecular: MT, methods
*F Factor
Gene Library
Molecular Sequence Data
Selection (Genetics)
Sequence Analysis, DNA: EC, economics
***Sequence Analysis, DNA: MT, methods**
CN 0 (F Factor)

. ISSN: 1046-7386.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
DNA: copy number, microarray; RNA: expression
IT Miscellaneous Descriptors
Meeting Abstract

L92 ANSWER 6 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:142903** BIOSIS
DN **PREV200200142903**
TI Response to neoadjuvant therapy for breast cancer by magnetic resonance imaging type, estrogen receptor status, grade, and comparative genomic hybridization.
AU Esserman, L. J. (1); Sudilovsky, D. (1); Kuo, W.-I. (1); **Gray, J. (1)**; Hylton, N. (1)
CS (1) Breast Care Center, University of California, San Francisco, San Francisco, CA USA
SO Breast Cancer Research and Treatment, (October, 2001) Vol. 69, No. 3, pp. 245. http://www.kluweronline.com/issn/0167-6806. print.
Meeting Info.: **24th Annual San Antonio Breast Cancer Symposium** San Antonio, Texas, USA December 10-13, 2001
ISSN: 0167-6806.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Radiation - Radiation and Isotope Techniques *06504
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Pathology, General and Miscellaneous - Diagnostic *12504
Pathology, General and Miscellaneous - Therapy *12512
Reproductive System - Physiology and Biochemistry *16504
Reproductive System - Pathology *16506
Pharmacology - General *22002
Pharmacology - Clinical Pharmacology *22005
Neoplasms and Neoplastic Agents - Diagnostic Methods *24001
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Therapeutic Agents; Therapy *24008
BC Hominidae 86215
IT Major Concepts
Gynecology (Human Medicine, Medical Sciences); Oncology (Human Medicine, Medical Sciences); Pharmacology; Radiology (Medical Sciences)
IT Parts, Structures, & Systems of Organisms
breast: reproductive system
IT Diseases
locally advanced breast cancer: neoplastic disease, reproductive system disease/female, therapy
IT Chemicals & Biochemicals
Her2 Ab [Her2 antibody]; adriamycin: antineoplastic - drug; cytoxan: antineoplastic - drug
IT Methods & Equipment
comparative genomic hybridization: analytical method; magnetic resonance imaging: Imaging Techniques, diagnostic method; neoadjuvant

therapy: efficacy, therapeutic method
IT Miscellaneous Descriptors
estrogen receptor status; treatment response; tumor diameter; tumor grade; **Meeting Abstract; Meeting Poster**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): female, patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 25316-40-9 (ADRIAMYCIN)
50-18-0 (CYTOXAN)

L92 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1996:555396** BIOSIS
DN **PREV199699277752**
TI Comparative genomic hybridization to arrayed DNA targets (CGHa) for high resolution analysis of DNA sequence copy number changes.
AU Pinkel, D. (1); Segraves, R. (1); Sudar, D.; Van Vliet, L.; Zhai, Y. (1); **Gray, J. W. (1)**; Albertson, D. G.
CS (1) Univ. Calif., San Francisco, CA USA
SO American Journal of Human Genetics, (1996) Vol. 59, No. 4 SUPPL., pp. A78.
Meeting Info.: **46th Annual Meeting of the American Society of Human Genetics** San Francisco, California, USA October 29-November 2, 1996
ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Microscopy Techniques - Cytology and Cytochemistry *01054
Cytology and Cytochemistry - General *02502
Genetics and Cytogenetics - General *03502
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Genetics; Methods and Techniques; Tumor Biology
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CANCER GENES; CANCER GENETICS; COMPARATIVE GENOMIC HYBRIDIZATION; DNA; GENETIC METHOD; **MEETING ABSTRACT**; **MEETING POSTER**; METHODOLOGY; MOLECULAR GENETICS; TUMOR BIOLOGY

L92 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1995:142045** BIOSIS
DN **PREV199598156345**
TI DNA copy number alterations in primary cutaneous malignant melanoma using comparative genomic hybridization.
AU White, W. L. (1); Thompson, C. T.; Halaban, R.; Khavari, R.; **Gray, J. W.**; Pinkel, D.
CS (1) Bowman Gray Sch. Med., Winston-Salem, NC USA
SO Modern Pathology, (1995) Vol. 8, No. 1, pp. 52A.
Meeting Info.: **Annual Meeting of the United States and Canadian Academy of Pathology** Toronto, Ontario, Canada March 11-17, 1995
ISSN: 0893-3952.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of**

Conferences, Congresses, Review Annuals 00520
Cytology and Cytochemistry - Human *02508
Clinical Biochemistry; General Methods and Applications *10006
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Pathology, General and Miscellaneous - Diagnostic *12504
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Integumentary System - Pathology *18506
Neoplasms and Neoplastic Agents - Diagnostic Methods *24001
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Biochemistry *24006
BC Hominidae *86215
IT Major Concepts
Cell Biology; Clinical Chemistry (Allied Medical Sciences); Dermatology (Human Medicine, Medical Sciences); Metabolism; Oncology (Human Medicine, Medical Sciences); Pathology
IT Miscellaneous Descriptors
CHROMOSOMAL ABERRATION; DIAGNOSTIC METHOD; **MEETING ABSTRACT**; TUMOR PROGRESSION
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L92 ANSWER 9 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1994:151247** BIOSIS
DN **PREV199497164247**
TI Use of comparative genomic hybridization to study genomic instability in neoplastic cells.
AU Roelofs, Helene; Lockett, Steve; Herman, Brian; **Gray, Joe W.**; Tlsty, Thea D.
CS Lineberger Comprehensive Cancer Center, University North Carolina, Chapel Hill, NC USA
SO Journal of Cellular Biochemistry Supplement, (1994) Vol. 0, No. 18 PART A, pp. 211.
Meeting Info.: **Keystone Symposium on Molecular Biology of Human Genetic Disease** Copper Mountain, Colorado, USA January 15-22, 1994
ISSN: 0733-1959.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Animal 02506
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Replication, Transcription, Translation 10300
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
IT Major Concepts
Genetics; Tumor Biology
IT Miscellaneous Descriptors
ANEUPLOIDY; CARCINOGENESIS; **MEETING ABSTRACT**

=> d all tot

L98 ANSWER 1 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2003:241548** BIOSIS
DN **PREV200300241548**
TI High resolution array **comparative genomic**

hybridization using archived prostate tissue to identify biomarkers of progression.

AU Paris, Pamela L. (1); Albertson, Donna (1); Andaya, Armann (1); Carroll, Peter (1); Fridlyand, Jane (1); Jain, Ajay (1); Kowbel, David (1); Pinkel, Dan (1); Watson, Vivienne (1); van Dekken, Herman; **Collins, Colin (1)**

CS (1) San Francisco, CA, USA USA

SO Journal of Urology, (April 2003, 2003) Vol. 169, No. 4 Supplement, pp. 435-436. print.
Meeting Info.: **98th Annual Meeting of the American Urological Association (AUA)** Chicago, IL, USA April 26-May 01, 2003 American Urological Association
. ISSN: 0022-5347.

DT **Conference**

LA English

CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Enzymes - General and Comparative Studies; Coenzymes *10802
Pathology, General and Miscellaneous - General *12502
Pathology, General and Miscellaneous - Diagnostic *12504
Urinary System and External Secretions - Pathology *15506
Reproductive System - Physiology and Biochemistry *16504
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Diagnostic Methods *24001
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007

BC Hominidae 86215

IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Oncology (Human Medicine, Medical Sciences); Urology (Human Medicine, Medical Sciences)

IT Parts, Structures, & Systems of Organisms
prostate: reproductive system

IT Diseases
prostate cancer: diagnosis, genetics, neoplastic disease, pathology, reproductive system disease/male, urologic disease

IT Chemicals & Biochemicals
prostate specific antigen [EC 3.4.21.77]

IT Alternate Indexing
Prostatic Neoplasms (MeSH)

IT Methods & Equipment
Gleason score: clinical techniques, diagnostic techniques; high resolution array **comparative genomic hybridization**: genetic techniques, laboratory techniques; microdissection: laboratory techniques

IT Miscellaneous Descriptors
carcinogenesis; clinical outcome; progression biomarkers; **Meeting Abstract**

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae): male, patient

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 2 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN **2002:616018** BIOSIS

DN **PREV200200616018**

TI Correlating array CGH with gene expression and sensitivity to drugs in a panel of 60 human cancer cell lines.

AU Bussey, K. J. (1); Chin, K.; Reinhold, W. C. (1); Lababidi, S. (1); Gwadry, F.; Scherf, U.; Ajay; Tonon, G.; Roschke, A.; Stover, K.; Kirsch, I.; Scudiero, D. A.; **Gray, J. W.**; Weinstein, J. N. (1)
CS (1) Laboratory of Molecular Pharmacology, National Cancer Institute, Bethesda, MD USA
SO American Journal of Human Genetics, (October, 2002) Vol. 71, No. 4 Supplement, pp. 200. http://www.journals.uchicago.edu/AJHG/home.html. print.
Meeting Info.: **52nd Annual Meeting of the American Society of Human Genetics** Baltimore, MD, USA October 15-19, 2002 American Society of Human Genetics
. ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Enzymes - General and Comparative Studies; Coenzymes *10802
Pathology, General and Miscellaneous - Therapy *12512
Blood, Blood-Forming Organs and Body Fluids - Blood, Lymphatic and Reticuloendothelial Pathologies *15006
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Therapeutic Agents; Therapy *24008
Neoplasms and Neoplastic Agents - Blood and Reticuloendothelial Neoplasms *24010
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology
IT Diseases
ALL [acute lymphoblastic leukemia]: blood and lymphatic disease, neoplastic disease; cancer: neoplastic disease
IT Chemicals & Biochemicals
L-asparaginase: antineoplastic - drug; asparagine synthetase; gene
IT Alternate Indexing
Neoplasms (MeSH)
IT Methods & Equipment
array CGH: analytical method
IT Miscellaneous Descriptors
DNA copy number; **Meeting Abstract**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 9015-68-3 (L-ASPARAGINASE)
9023-69-2 (ASPARAGINE SYNTHETASE)

L98 ANSWER 3 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:1365** BIOSIS
DN **PREV200200001365**
TI Genetic profiling of non-small cell lung cancer using array-**Comparative Genomic hybridization.**
AU Massion, Pierre P. (1); Kuo, Wen-Lin (1); Chin, Koei (1); Treseler, Patrick (1); Chen, Chira (1); Polikoff, Daniel (1); Pinkel, Daniel (1); Albertson, Donna (1); Jain, Ajay (1); Jablons, David (1); **Gray, Joe (1)**
CS (1) UCSF, San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting,** (March, 2001) Vol. 42, pp. 745. print.

Meeting Info.: **92nd Annual Meeting of the American Association for Cancer Research** New Orleans, LA, USA March 24-28, 2001
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Respiratory System - Pathology *16006
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Oncology (Human Medicine, Medical Sciences)
IT Diseases
non-small cell lung cancer: neoplastic disease, respiratory system disease
IT Alternate Indexing
Lung Neoplasms (MeSH); Carcinoma, Non-Small-Cell Lung (MeSH)
IT Methods & Equipment
array-**Comparative Genomic Hybridization:**
detection method, genetic method
IT Miscellaneous Descriptors
cancer genetic profiling; cancer genetics; **Meeting Abstract**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 4 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:1362** BIOSIS
DN **PREV200200001362**
TI Genome wide screening of gene copy number changes on the NCI 60 cell lines using array CGH.
AU Chin, Koei (1); Kuo, Wen-Lin; Jain, Ajay; Albertson, Donna; Pinkel, Dan; Scherf, Uwe; Reinhold, William C.; Weinstein, John N.; **Gray, Joe W.**
CS (1) National Cancer Institute, Bethesda, MD USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2001) Vol. 42, pp. 744. print.
Meeting Info.: **92nd Annual Meeting of the American Association for Cancer Research** New Orleans, LA, USA March 24-28, 2001
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - General *10060
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Mammalia - Unspecified 85700
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Tumor Biology
IT Methods & Equipment
array **comparative genomic hybridization:**
detection method, genetic method, screening method

IT Miscellaneous Descriptors
gene copy number changes: genome wide screening; **Meeting Abstract**
CO National Cancer Institute
ORGN Super Taxa
Mammalia: Vertebrata, Chordata, Animalia
ORGN Organism Name
mammal (Mammalia): NCI 60 cell lines
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates

L98 ANSWER 5 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2001:440426** BIOSIS
DN **PREV200100440426**
TI **Genomic** profiling of ovarian cancer by array **comparative genomic hybridization.**
AU Kuo, Wen-Lin (1); Polikoff, Daniel; Yamada, Kyosuke; Glenn, Pat; Zaloudek, Chuck; Smith-McCune, Karen; Mills, Gordon B.; Lu, Karen; Deavers, Mike; Shaw, Pat; **Collins, Colin**; Hamilton, Greg; Jain, Ajay; Brown, Nils; Albertson, Donna; Pinkel, Dan; **Gray, Joe W.**
CS (1) MD Anderson Cancer Center, Houston, TX USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2001) Vol. 42, pp. 429. print.
Meeting Info.: **92nd Annual Meeting of the American Association for Cancer Research** New Orleans, LA, USA March 24-28, 2001
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Reproductive System - Physiology and Biochemistry *16504
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques; Reproductive System (Reproduction); Tumor Biology
IT Parts, Structures, & Systems of Organisms
chromosome 16: locus q22-ter; chromosome 20: locus q13; chromosome 3: locus q22, locus q26; chromosome 8: q arm; ovary: reproductive system
IT Diseases
gene abnormality: genetic disease; serous ovarian cancer: neoplastic disease, reproductive system disease/female
IT Methods & Equipment
array **comparative genomic hybridization:** gene profiling method
IT Miscellaneous Descriptors
Meeting Abstract
GEN AIB1 gene; BBC gene; BCL6 gene; CACNA1D gene; CMYC gene: amplification; CTSB gene; CYP24 gene; E-cadherin gene; EVI1 gene; FHIT gene; LBL gene; PIK3CA gene; PIK3CB gene; RHO gene; SPO11 gene; SST gene; TERC gene; THPO gene; THRB gene; VHL gene; ZNF217 gene; ZNF9 gene

L98 ANSWER 6 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2001:84904** BIOSIS
DN **PREV200100084904**
TI Changes in leg ulcers treated with compressive support.
AU Roberts, G. H. (1); Hammad, L. (1); **Collins, C. S. (1)**; Creevy, J. (1); Shearman, C. P. (1); Mani, R. (1)
CS (1) Southampton University Hospitals Trust, Tremona Road, Southampton, SO16 6YD UK

SO Wound Repair and Regeneration, (September October, 2000) Vol. 8, No. 5, pp. A430. print.
Meeting Info.: **Tenth Annual Meeting of the European Tissue Repair Society** Brussels, Belgium May 24-27, 2000
ISSN: 1067-1927.
DT **Conference**
LA English
SL English
CC Integumentary System - Pathology *18506
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Pathology, General and Miscellaneous - Therapy *12512
Cardiovascular System - Heart Pathology *14506
Cardiovascular System - Blood Vessel Pathology *14508
BC Hominidae 86215
IT Major Concepts
Cardiovascular Medicine (Human Medicine, Medical Sciences); Dermatology (Human Medicine, Medical Sciences)
IT Diseases
venous leg ulcers: compressive support-induced changes, integumentary system disease, vascular disease
IT Methods & Equipment
Profore compressive bandage treatment: therapeutic method, venous leg ulcer changes
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 7 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:275363 BIOSIS
DN PREV200000275363
TI Gene-based array CGH construction and tumor genome analysis.
AU Polikoff, Daniel (1); Kuo, W.-L.; Massion, P.; Chin, K.; **Collins, C.**; Yue, P.; Myambo, K.; Riedell, L.; Wernick, M.; McCue, C.; Hamilton, G.; Glenn, P.
CS (1) CA Institute of Technology, Pasadena, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 726. print..
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research.** San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC Neoplasms and Neoplastic Agents - General *24002
Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
Reproductive System - General; Methods *16501
Endocrine System - General *17002
Respiratory System - General; Methods *16001
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology
IT Diseases

breast cancer: neoplastic disease, reproductive system disease/female; lung cancer: neoplastic disease, respiratory system disease; ovarian cancer: neoplastic disease, reproductive system disease/female
IT Alternate Indexing
Breast Neoplasms (MeSH); Lung Neoplasms (MeSH); Ovarian Neoplasms (MeSH)
IT Methods & Equipment
FISH [fluorescence in-situ **hybridization**]: genetic method; **comparative genomic hybridization** [CGH]: gene-based array, genetic method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 8 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:275352 BIOSIS
DN PREV200000275352
TI Oligonucleotide-array-based **comparative genomic hybridization.**
AU Baldocchi, Russ A. (1); Glynne, Richard J.; Kowbel, Dave; Tom, Ed; Segraves, Rick; Albertson, Donna; Pinkel, Dan; **Collins, Colin**; Mack, David H.; **Gray, Joe W.**
CS (1) Eos Biotech, Inc, S.San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 724. print..
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research**. San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC Neoplasms and Neoplastic Agents - General *24002
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Reproductive System - General; Methods *16501
Biophysics - General Biophysical Studies *10502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Reproductive System (Reproduction); Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female
IT Alternate Indexing
Breast Neoplasms (MeSH)
IT Methods & Equipment
comparative genomic hybridization: genetic method, oligonucleotide array-based
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
MCF-7 cell line (Hominidae): human breast cancer cells
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 9 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:275314 BIOSIS
DN PREV200000275314
TI p53 inactivation under natural selection in brain tumor progression without significant chromosomal instability.
AU Lu, Xiangdong (1); Magrane, G.; **Gray, J.**; Van Dyke, T.
CS (1) Univ of CA at San Francisco, San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 717-718. print..
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research.** San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC Neoplasms and Neoplastic Agents - General *24002
Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - General *10060
Nervous System - General; Methods *20501
Biophysics - General Biophysical Studies *10502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Muridae 86375
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Nervous System (Neural Coordination); Tumor Biology
IT Diseases
brain tumor: neoplastic disease, nervous system disease, progression
IT Chemicals & Biochemicals
p53 tumor suppressor protein: chromosomal instability, inactivation
IT Alternate Indexing
Brain Neoplasms (MeSH)
IT Methods & Equipment
comparative genomic hybridization: genetic method; in-situ **hybridization:** genetic method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae)
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L98 ANSWER 10 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2000:216415** BIOSIS
DN **PREV200000216415**
TI Genomic copy number changes measured by CGH and quantitative PCR are correlated with clinical outcome in ovarian cancer patients.
AU Suzuki, Seiji (1); Ginzinger, David; Godfrey, Tony; Moore, Dan; Barclay, John; Powell, Bethan; Pinkel, Dan; Zaloudek, Charles; Berchuck, Andrew; **Gray, Joe**
CS (1) Duke Univ, Raleigh-Durham, NC USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 419.
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research.** San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English

SL English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Reproductive System - General; Methods *16501
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Reproductive System (Reproduction); Tumor Biology
IT Diseases
ovarian cancer: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals
chromosome 1; chromosome 13; chromosome 16; chromosome 17; chromosome 18; chromosome 20; chromosome 3; chromosome 4; chromosome 7; chromosome 8; chromosome X
IT Alternate Indexing
Ovarian Neoplasms (MeSH)
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification, analytical method, in-situ recombinant gene expression detection, sequencing techniques; **comparative genomic hybridization:**
analytical method
IT Miscellaneous Descriptors
chromosomal alterations; disease survival; genomic copy number; outcome; tumor grade; tumor stage; **Meeting Abstract**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): female, patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 11 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2000:216412** BIOSIS
DN **PREV200000216412**
TI Comparison of p53 mutations and genome copy number abnormalities measured using CGH in human breast cancers.
AU Chin, K. (1); Moore, D.; Erikstein, B.; Karresen, R.; Lonning, P. E.; Boerresen-Dale, A.-L.; **Gray, J. W.**
CS (1) Haukeland Hospital, Oslo Norway
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 418.
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research.** San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Reproductive System - General; Methods *16501
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Respiratory System (Respiration); Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals

chromosome 12; chromosome 13; chromosome 16; chromosome 17; chromosome 18; chromosome 20; chromosome 3; chromosome 5; chromosome 8; chromosome X; p53
IT Alternate Indexing
Breast Neoplasms (MeSH)
IT Methods & Equipment
comparative genomic hybridization:
analytical method; **genome**-wide survival association analysis: analytical method
IT Miscellaneous Descriptors
disease survival; gene mutations; genome copy number; tumor stage; **Meeting Abstract**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 12 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:216406 BIOSIS
DN PREV200000216406
TI Measurement of DNA sequence copy number alterations by array CGH in human and mouse genomes.
AU Albertson, Donna G. (1); Segraves, Richard (1); Huey, Bing (1); Zhang, Xiao Xiao (1); Palmer, Joel (1); Blackwood, Stephanie (1); Snijders, Antoine (1); Hamilton, Gregory (1); Hindle, Anna Katharine (1); Livezey, Kristin (1); **Gray, Joe W. (1)**; Pinkel, Daniel (1)
CS (1) Univ of CA, San Francisco, San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2000) No. 41, pp. 417.
Meeting Info.: **91st Annual Meeting of the American Association for Cancer Research**. San Francisco, California, USA April 01-05, 2000
ISSN: 0197-016X.
DT **Conference**
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - General *10060
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
Muridae 86375
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology
IT Chemicals & Biochemicals
BAC clones; candidate driver oncogenes; disease genes
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; **comparative genomic hybridization**: analytical method
IT Miscellaneous Descriptors
DNA sequence copy number; **Meeting Abstract**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae); mouse (Muridae)
ORGN Organism Superterms

Animals; Chordates; Humans; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Primates; Rodents; Vertebrates

L98 ANSWER 13 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:133691 BIOSIS
DN PREV200000133691
TI Oligonucleotide-array-based **comparative genomic hybridization.**
AU Baldocchi, R. A. (1); Glynne, R. J.; Kowbel, D.; Tom, E.; **Collins, C.**; Mack, D. H.; **Gray, J. W.**
CS (1) University of California at San Francisco Cancer Center, San Francisco, CA, 94143-0808 USA
SO Breast Cancer Research and Treatment., (1999) Vol. 57, No. 1, pp. 33. Meeting Info.: **22nd Annual San Antonio Breast Cancer Symposium** San Antonio, Texas, USA December 8-11, 1999 ISSN: 0167-6806.
DT **Conference**
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female, tumor development
IT Chemicals & Biochemicals
AIBC-1 gene (Hominidae): tumor development role; BRCA-2 gene (Hominidae): tumor development role; CCND-1 gene (Hominidae): tumor development role; ErbB-2 gene (Hominidae): tumor development role; MYC oncogene (Hominidae): tumor development role; ZINF-217 gene (Hominidae): tumor development role; p53 gene (Hominidae): tumor development role
IT Alternate Indexing
Breast Neoplasms (MeSH)
IT Methods & Equipment
oligonucleotide aray-based **comparative genomic hybridization:** genetic method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): female, patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 14 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1999:506809** BIOSIS
DN **PREV199900506809**
TI High throughput mapping of Cri du Chat deletions on 5p using **comparative genomic hybridization** to DNA microarrays.
AU Zhang, X. (1); Segraves, R. (1); Bolund, L.; Yang, H. M.; Niebuhr, E.; **Gray, J. (1)**; Albertson, D. (1); Pinkel, D. (1)
CS (1) Cancer Center, UCSF, San Francisco, CA USA
SO American Journal of Human Genetics, (Oct., 1999) Vol. 65, No. 4, pp. A364.

Meeting Info.: **49th Annual Meeting of the American Society of Human Genetics** San Francisco, California, USA October 19-23, 1999 The American Society of Human Genetics
. ISSN: 0002-9297.
DT **Conference**
LA English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Medical Genetics (Allied Medical Sciences)
IT Chemicals & Biochemicals
DNA: microarray; 5p: Cri du Chat deletion
IT Methods & Equipment
comparative genomic hybridization:
mapping method; high throughput mapping: mapping method
IT Miscellaneous Descriptors
constitutional aberration; diagnostic capability; **Meeting Abstract; Meeting Poster**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 15 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1998:196225 BIOSIS
DN PREV199800196225
TI Analysis of DNA sequence copy number variation in breast cancer using **comparative genomic hybridization** to DNA microarrays.
AU Albertson, D. G. (1); Segraves, R.; Sudar, D. (1); Clark, S.; **Collins, C. (1)**; Chen, C.; Kuo, W.-L.; Kowbel, D. (1); Dairkee, S. H.; Poole, I.; **Gray, J. W. (1)**; Pinkel, D. (1)
CS (1) E.O. Lawrence Berkeley National Lab., Berkeley, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 1998) Vol. 39, pp. 345.
Meeting Info.: **89th Annual Meeting of the American Association for Cancer Research** New Orleans, Louisiana, USA March 28-April 1, 1998 American Association for Cancer Research
. ISSN: 0197-016X.
DT **Conference**
LA English
CC Genetics and Cytogenetics - Human *03508
Reproductive System - General; Methods *16501
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Genetics; Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals
DNA
IT Methods & Equipment
comparative genomic hybridization:
analytical method, genetic method
IT Miscellaneous Descriptors
sequence copy number variation; **Meeting Abstract**

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L98 ANSWER 16 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1998:190153 BIOSIS
DN PREV199800190153
TI High resolution analysis of DNA copy number variation using **comparative genomic hybridization** to DNA microarrays.
AU Pinkel, D. (1); Segraves, R.; Sudar, D.; Poole, S. Clark I.; Jones, A.; **Collins, C.**; Zou, Y.; Dairkee, S.; **Gray, J.**; Albertson, D. (1)
CS (1) Univ. Calif. San Francisco, San Francisco, CA USA
SO Cytometry, (1998) No. SUPPL. 9, pp. 24-25.
Meeting Info.: **XIX International Congress of the International Society for Analytical Cytology** Colorado Springs, Colorado, USA February 28-March 5, 1998 International Society for Analytical Cytology . ISSN: 0196-4763.
DT **Conference**
LA English
CC Microscopy Techniques - General and Special Techniques *01052
Cytology and Cytochemistry - General *02502
Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA: copy number variation, high resolution analysis, microarray
IT Methods & Equipment
comparative genomic hybridization: detection method
IT Miscellaneous Descriptors
Meeting Abstract

L98 ANSWER 17 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1998:190136 BIOSIS
DN PREV199800190136
TI Genomics, molecular cytogenetics and cytometry.
AU **Gray, Joe W. (1)**
CS (1) UCSF Cancer Cent., Univ. Calif., San Francisco, CA USA
SO Cytometry, (1998) No. SUPPL. 9, pp. 20.
Meeting Info.: **XIX International Congress of the International Society for Analytical Cytology** Colorado Springs, Colorado, USA February 28-March 5, 1998 International Society for Analytical Cytology . ISSN: 0196-4763.
DT **Conference**
LA English
CC Cytology and Cytochemistry - General *02502
Microscopy Techniques - General and Special Techniques *01052
Genetics and Cytogenetics - General *03502
Biophysics - General Biophysical Studies *10502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Cell Biology; Methods and Techniques; Molecular Genetics (Biochemistry

and Molecular Biophysics)
IT Methods & Equipment
comparative genomic hybridization:
analytical method; cytometry: analytical method, cytological method; fluorescence in situ **hybridization** [FISH]: analytical method; quantitative PCR [quantitative polymerase chain reaction]: analytical method
IT Miscellaneous Descriptors
genomics; molecular cytogenetics; **Meeting Abstract**

L98 ANSWER 18 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:397422 BIOSIS
DN PREV199699119778
TI Genetic progression in breast cancer; chaos and consistency.
AU **Gray, J. W. (1)**; Hwang, S.; Godfrey, T. (1); Kowbel, D.; Kallioniemi, O.; Tanner, M.; Isola, J.; Pinkel, F. D. (1); Waldman, F. (1); Rommens, J.; **Collins, C.**
CS (1) Univ. California, San Francisco, CA USA
SO Journal of Histochemistry and Cytochemistry, (1996) Vol. 44, No. 7, pp. 783.
Meeting Info.: **47th Annual Meeting of the Histochemical Society** Bethesda, Maryland, USA August 2-3, 1996
ISSN: 0022-1554.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Microscopy Techniques - Cytology and Cytochemistry *01054
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics; Methods and Techniques; Oncology (Human Medicine, Medical Sciences); Reproductive System (Reproduction)
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CHROMOSOMAL ABERRATION; **COMPARATIVE GENOMIC HYBRIDIZATION**; DIAGNOSIS; FLUORESCENCE IN-SITU **HYBRIDIZATION**; **MEETING ABSTRACT**; PROGNOSIS; THERAPY DEVELOPMENT
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 19 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:476679 BIOSIS
DN PREV199598490979
TI Genetic analyses of borderline ovarian tumor using **comparative genomic hybridization.**
AU Iwabuchi, Hiroshi (1); Sakunaga, Hotaka; Sakamoto, Masaru; Yang-Feng, Teresa L.; Pinkel, Dan (1); **Gray, Joe W. (1)**
CS (1) Dep. Lab. Med., Univ. Calif., San Francisco, CA USA
SO American Journal of Human Genetics, (1995) Vol. 57, No. 4 SUPPL., pp. A67.
Meeting Info.: **45th Annual Meeting of the American Society of Human Genetics** Minneapolis, Minnesota, USA October 24-28, 1995
ISSN: 0002-9297.
DT **Conference**

LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - General *24002
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics; Oncology (Human Medicine, Medical Sciences); Reproductive System (Reproduction)
IT Miscellaneous Descriptors
CHROMOSOME; COPY NUMBER ABNORMALITY; **MEETING ABSTRACT ; MEETING POSTER**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 20 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:185532 BIOSIS
DN PREV199598199832
TI Genetic progression model in ovarian cancer with **comparative genomic hybridization** (CGH.
AU Iwabuchi, H. (1); Sakunaga, H.; Sakamoto, M.; Yang-Feng, T. L.; Pinkel, D.; **Gray, J. W.**
CS (1) Dep. Lab. Med., Univ. Calif., San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (1995) Vol. 36, No. 0, pp. 226.
Meeting Info.: **Eighty-sixth Annual Meeting of the American Association for Cancer Research** Toronto, Ontario, Canada March 18-22, 1995
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Genetics and Cytogenetics - Human *03508
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Genetics; Oncology (Human Medicine, Medical Sciences); Reproductive System (Reproduction)
IT Miscellaneous Descriptors
CHROMOSOMAL ABERRATION; **MEETING ABSTRACT**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 21 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:185307 BIOSIS
DN PREV199598199607
TI CGH analysis of mammary tumors from Wnt-1 transgenic mice demonstrates a dependence of chromosome stability on p53 status.

AU Shi, Y.-P. (1); Godley, L. A.; Donehower, L. A.; Varmus, H. E.; **Gray, J. W. (1)**; Pinkel, D. (1)
CS (1) Dep. Lab. Med., Univ. California, San Francisco, CA 94143 USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (1995) Vol. 36, No. 0, pp. 188.
Meeting Info.: **Eighty-sixth Annual Meeting of the American Association for Cancer Research** Toronto, Ontario, Canada March 18-22, 1995
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biophysics - General Biophysical Techniques 10504
Biophysics - Molecular Properties and Macromolecules 10506
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Muridae *86375
IT Major Concepts
Cell Biology; Genetics; Reproductive System (Reproduction); Tumor Biology
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CARCINOGENESIS; **COMPARATIVE GENOMIC HYBRIDIZATION; MEETING ABSTRACT**
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
Muridae (Muridae)
ORGN Organism Superterms
animals; chordates; mammals; nonhuman vertebrates; nonhuman mammals; rodents; vertebrates

L98 ANSWER 22 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1994:526383 BIOSIS
DN PREV199497539383
TI Resource for molecular cytogenetic analysis.
AU Kuo, W.-L. (1); **Collins, C.**; Weier, U.; Sudar, D.; Mullikin, J.; Lockett, S.; Riedell, L. (1); Yue, P. (1); Kowbel, D.; Shadravan, F.; Pinkel, D. (1); **Gray, J. (1)**
CS (1) LBL/USCF Resource Mol. Cytogenetics, Dep. Lab. Med., Univ. Calif., San Francisco, CA USA
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A372.
Meeting Info.: **44th Annual Meeting of the American Society of Human Genetics** Montreal, Quebec, Canada October 18-22, 1994
ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Biophysics - Molecular Properties and Macromolecules *10506
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics
IT Miscellaneous Descriptors
COMPARATIVE GENOMIC ANALYSIS; FLUORESCENCE IN SITU

HYBRIDIZATION; MEETING ABSTRACT; MOLECULAR GENETICS; PHYSICAL MAP
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 23 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1994:524526 BIOSIS
DN PREV199497537526
TI Model of genetic progression in ovarian cancer with **comparative genomic hybridization.**
AU Iwabuchi, H. (1); Sakamoto, M. (1); Sakunaga, H. (1); Yang-Feng, T. L.; **Gray, J. W. (1)**
CS (1) Dep. Lab. Med., Univ. Calif. San Francisco, CA USA
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A60.
Meeting Info.: **44th Annual Meeting of the American Society of Human Genetics** Montreal, Quebec, Canada October 18-22, 1994
ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics; Oncology (Human Medicine, Medical Sciences); Reproductive System (Reproduction)
IT Miscellaneous Descriptors
CHROMOSOMAL ABERRATION; **MEETING ABSTRACT; MEETING POSTER;** TUMOR PROGRESSION
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 24 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1994:289270 BIOSIS
DN PREV199497302270
TI Genetic events underlying breast cancer progression analyzed by **comparative genomic hybridization.**
AU Kallioniemi, O.-P. (1); Isola, J.; Kallioniemi, A.; Tanner, M.; Stokke, T.; Heintz, M.; **Collins, C.**; Smith, H. S.; Fuqua, S.; Pinkel, D.; **Gray, J. W.**; Waldman, F.
CS (1) Univ. Tampere, 33521 Tampere Finland
SO **Proceedings of the American Association for Cancer Research Annual Meeting,** (1994) Vol. 35, No. 0, pp. 250.
Meeting Info.: **85th Annual Meeting of the American Association for Cancer Research** San Francisco, California, USA April 10-13, 1994
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human 02508
Genetics and Cytogenetics - Human *03508

Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Genetics; Oncology (Human Medicine, Medical Sciences); Reproductive System (Reproduction)
IT Miscellaneous Descriptors
CARCINOGENESIS; **MEETING ABSTRACT**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L98 ANSWER 25 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1993:378583 BIOSIS
DN PREV199345050008
TI Analysis of genetic aberrations in ovarian cancers using **comparative genomic hybridization.**
AU Sakamoto, M. (1); Sakunaga, H. (1); Yang-Feng, T.; Li, S.; Kallioniemi, A. (1); Kallioniemi, O. (1); Pinkel, D. (1); **Gray, J. (1)**
CS (1) Univ. Calif., San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (1993) Vol. 34, No. 0, pp. 210.
Meeting Info.: **84th Annual Meeting of the American Association for Cancer Research** Orlando, Florida, USA May 19-22, 1993
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Biochemical Studies - General 10060
Pathology, General and Miscellaneous - Diagnostic *12504
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Diagnostic Methods *24001
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics; Oncology (Human Medicine, Medical Sciences); Pathology; Reproductive System (Reproduction)
IT Miscellaneous Descriptors
ABSTRACT; CHROMOSOME 19; DIAGNOSTIC METHOD; GENE COPY NUMBER
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 17:02:04 ON 15 JUL 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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L66 ANSWER 2 OF 3 MEDLINE
AN **94063908** MEDLINE
DN **94063908** PubMed ID: **8244381**
TI Ordered shotgun sequencing, a strategy for integrated mapping and sequencing of YAC clones.
AU Chen E Y; Schlessinger D; Kere J
CS Advanced Center for Genetic Technology, Applied Biosystems, Inc., Foster City, California 94404.
NC HG00247 (NHGRI)
SO GENOMICS, **(1993 Sep)** 17 (3) 651-6.
Journal code: 8800135. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199312
ED Entered STN: 19940201
Last Updated on STN: 19980206
Entered Medline: 19931229
AB Ordered shotgun sequencing proposes to organize the mapping and sequencing of YACs with a hierarchical strategy that incorporates a feedback loop. Building on current protocols, a YAC is subcloned into plasmids, plasmid insert ends are sequenced, and the sequences are overlapped to create a partial map. Complete sequencing then starts with plasmids whose **end-sequence** tracts have overlapped, but to a minimal extent. The next plasmids to be sequenced are again selected for least overlap, striking out progressively to span the YAC with minimal directed gap-filling. Simulations support its feasibility and indicate that during the generation of the complete sequence, the approach facilitates the early choice of regions for selective sequencing, for example, for coding units. The sequencing of plasmids would also require less redundancy, and discriminate repetitive sequences more easily, than random sequencing across larger clones. The overall effort scales with YAC size and can be further reduced by additional mapping information.
CT Check Tags: Human; Support, U.S. Gov't, P.H.S.
***Chromosome Mapping: MT, methods**
***Chromosomes, Artificial, Yeast**
Cloning, Molecular
Computer Simulation
Evaluation Studies
Genome, Human
Models, Genetic
Plasmids: GE, genetics
***Sequence Analysis, DNA: MT, methods**
Sequence Tagged Sites
CN 0 (Chromosomes, Artificial, Yeast); 0 (Plasmids)

L66 ANSWER 3 OF 3 MEDLINE
AN **90272391** MEDLINE
DN **90272391** PubMed ID: **2161516**
TI A novel, rapid method for the isolation of **terminal sequences** from yeast artificial chromosome (YAC) clones.
AU Riley J; Butler R; Ogilvie D; Finniear R; Jenner D; Powell S; Anand R; Smith J C; Markham A F
CS ICI Pharmaceuticals, Biotechnology Department, Macclesfield, Cheshire, UK.
SO NUCLEIC ACIDS RESEARCH, **(1990 May 25)** 18 (10) 2887-90.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X52166; GENBANK-X52167
EM 199007

ED Entered STN: 19900810
Last Updated on STN: 19900810
Entered Medline: 19900711

AB The recent development of yeast artificial chromosome (YAC) vectors has provided a system for cloning fragments that are over ten times larger than those that can be cloned in more established systems. We have developed a method for the rapid isolation of **terminal sequences** from YAC clones. The YAC clone is digested with a range of restriction enzymes, a common linker is ligated to the DNA fragments and **terminal sequences** are amplified using a vector specific primer and a linker specific primer. Sequence data derived from these terminal specific products can be used to design primers for a further round of screening to isolate overlapping clones. The method also provides a convenient method of generating Sequence Tagged Sites for the mapping of complex genomes.

CT **Base Sequence**
Chromosomes, Fungal
Cloning, Molecular
DNA Restriction Enzymes
Gene Amplification
*Gene Library
*Genetic Techniques
Genetic Vectors
Molecular Sequence Data
Restriction Mapping
Saccharomyces cerevisiae: GE, genetics

CN 0 (Genetic Vectors); EC 3.1.21 (DNA Restriction Enzymes)

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=> d his

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               SET COST OFF

     FILE 'WPIX' ENTERED AT 13:39:03 ON 16 JUL 2003
               E WO2001075856/PN
L1             1 S E3
               E WO2001092558/PN
L2             1 S E3
               E COLLINS C/AU
L3           129 S E3-E20
               E GRAY J/AU
L4           130 S E3,E21
               E VOLIK S/AU
L5             3 S E3,E4
L6         27092 S (B04-E01 OR C04-E01 OR B04-B04A1 OR C04-B04A1)/MC
L7         13925 S (B04-E05 OR C04-E05)/MC
L8          1664 S (B11-C08F OR C11-C08F OR B11-C08F1 OR C11-C08F1 OR B11-C08G O
L9         16893 S (B12-K04F OR C12-K04F)/MC
L10        15771 S D05-H12/MC
L11          864 S D05-H12D/MC
L12        13766 S D05-H12D1/MC
L13        14157 S D05-H18?/MC
L14           46 S L3-L5 AND L6-L12
L15           52 S C12Q/IC,ICM,ICS AND L3-L5
L16           55 S L14,L15
L17          194 S L3-L5 NOT L16
L18           55 S L1,L2,L16
L19            2 S L18 AND G06F/IC,ICM,ICS,ICA,ICI
L20            3 S L18 AND T?/MC
L21            5 S L19,L20
L22            4 S L21 NOT PRINT HEAD/TI
L23           50 S L18 NOT L19-L22
               SEL DN AN 8 10 20 40
L24            4 S E1-E8
L25            8 S L22,L24 AND L1-L14

     FILE 'WPIX' ENTERED AT 14:08:52 ON 16 JUL 2003

     FILE 'DPCI' ENTERED AT 14:09:55 ON 16 JUL 2003
               E WO2001092558/PN
L26            1 S E3

     FILE 'DPCI' ENTERED AT 14:10:25 ON 16 JUL 2003

     FILE 'WPIX' ENTERED AT 14:11:07 ON 16 JUL 2003
L27            2 S (US5830645 OR US6013439)/PN
L28            1 S L27 NOT L25

     FILE 'WPIX' ENTERED AT 14:11:35 ON 16 JUL 2003

     FILE 'MEDLINE' ENTERED AT 14:12:05 ON 16 JUL 2003
L29            1 S ALTSCHUL ?/AU AND 1990/PY AND (215 AND 403)/SO

     FILE 'MEDLINE' ENTERED AT 14:12:55 ON 16 JUL 2003
               E CHROMOSOMES/CT
               E E3+ALL
L30       143086 S E17+NT
               E CHROMOSOM/CT
               E E6+ALL
               E E2+ALL
L31        88566 S E8+NT
L32       189199 S L30,L31
               E MOLECULAR SEQUENCE/CT
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                E E4+ALL
L33       374736 S E5
L34       335581 S E30+NT
                E E76+ALL
L35        34652 S E4
L36        38406 S L32 AND L33-L35
                E SEQUENCE ANALYSIS/CT
                E E3+ALL
L37        68649 S E4+NT
L38         3995 S L36 AND L37
L39          355 S L32 AND (END OR TERMINAL)()SEQUENC?
L40         8126 S L33-L35 AND (END OR TERMINAL)()SEQUENC?
L41         1352 S L37 AND (END OR TERMINAL)()SEQUENC?
L42         7622 S L39-L41 AND PY<=2000
L43          297 S L42 AND L32
                E CONTIG MAPPING/CT
                E E3+ALL
                E E8+ALL
                E E4+ALL
L44        93240 S E4+NT
L45          690 S L44 AND L42
L46          146 S L43 AND L45
L47         7322 S L42 AND L1./CT
L48          225 S L47 AND L43
L49          113 S L47 AND L46
                E CLONING/CT
                E E9+ALL
L50       117415 S E4+NT
L51       102339 S L50 AND PY<=2000
L52         1934 S L51 AND (END OR TERMINAL)()SEQUENC?
L53          130 S L52 AND L32
                E GENOME/CT
                E E3 ALL
                E GENOME/CT
                E E3+ALL
L54        43036 S E6+NT
                E E5+ALL
L55          129 S L52 AND L54
L56          378 S L52 AND E4+NT
L57          428 S L55,L56
L58           72 S L49 AND L50
L59          366 S END SEQUENC? AND PY<=2000
L60        10683 S TERMINAL SEQUENC? AND PY<=2000
L61           81 S L59 AND L32
L62          217 S L60 AND L32
                SEL DN AN L61 32 66
L63            2 S L61 AND E1-E6
L64          216 S L62 NOT L61
                SEL DN AN 140 L64
L65            1 S L64 AND E7-E9
L66            3 S L63,L65 AND L30-L65

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